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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification: <b>C12Q 1/68</b>	<b>A3</b>	(11) International Publication Number: <b>WO 00/15779</b>
		(43) International Publication Date: 23 March 2000 (23.03.2000)

(21) International Application Number: <b>PCT/US99/21291</b>	<b>Published</b>
(22) International Filing Date: 15 September 1999 (15.09.1999)	
(30) Priority Data: 60/100,327 15 September 1998 (15.09.1998) US	
(60) Parent Application or Grant YALE UNIVERSITY {/}: (). LIZARDI, Paul, M. {/}; (). PABST, Patrea, L.; ().	

(54) Title: MOLECULAR CLONING USING ROLLING CIRCLE AMPLIFICATION

(54) Titre: CLONAGE MOLECULAIRE A AMPLIFICATION SELON LE MODELE DU CERCLE ROULANT

## (57) Abstract

Disclosed are reagents and a method for efficient in vitro molecular cloning of nucleic acid molecules of interest. Because the method is entirely in vitro, it can be automated and scaled-up in ways that are not possible in cell-based molecular cloning. The method involves insertion of a nucleic acid molecule of interest in a linear vector to form a circular vector where one strand is continuous and the other strand is discontinuous. The continuous strand of the circular vector is then amplified by rolling circle replication, amplifying the inserted nucleic acid molecule in the process. The amplification is rapid and efficient since it involves a single, isothermal reaction that replicates the vector sequences exponentially. The amplification process is amenable to automation where multiple reactions are carried out simultaneously in a small area. The amplified nucleic acid can be used for any purpose and in any manner that nucleic acid cloned or amplified by known methods can be used. This includes sequencing, probing, restriction analysis, subcloning, transcription, hybridization or denaturation analysis, further amplified, and storage for future use or analysis.

## (57) Abrégé

L'invention concerne des réactifs et un procédé permettant d'assurer un clonage moléculaire in vitro de molécules d'acides nucléiques déterminées. Etant entièrement in vitro, le procédé peut être automatisé et étendu selon des modalités qu'il est impossible de mettre en oeuvre avec le clonage moléculaire à base cellulaire. Le procédé consiste à insérer la molécule d'acide nucléique concernée dans un vecteur linéaire, de manière à former un vecteur circulaire dans lequel un brin est continu et l'autre brin est discontinu. Le brin continu est ensuite amplifié selon le modèle du cercle roulant, ce qui permet d'amplifier par la même occasion la molécule d'acide nucléique. L'amplification est rapide et efficace car elle fait intervenir une réaction isothermique unique qui assure la réplication exponentielle des séquences du vecteur. Le procédé peut être automatisé lorsque plusieurs réactions sont conduites simultanément dans une zone de taille réduite. L'acide nucléique amplifié peut être utilisé à toute fin et de façon quelconque dans l'éventail d'utilisation connu de l'acide nucléique cloné ou amplifié, y compris le séquençage, la détermination de sondes, l'analyse de restriction, le sous-clonage, la transcription, l'analyse d'hybridation ou de dénaturation, le complément d'amplification et le stockage pour utilisation ou analyse ultérieure.

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# INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 99/21291

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 19193 A (UNIV YALE) 29 May 1997 (1997-05-29) the whole document	1-5, 49-51 6-48, 52
X	LIZARDI P M ET AL: "MUTATION DETECTION AND SINGLE-MOLECULE COUNTING USING ISOTHERMAL ROLLING-CIRCLE AMPLIFICATION" NATURE GENETICS, US, NEW YORK, NY, vol. 19, no. 3, July 1998 (1998-07), pages 225-232, XP000856939 ISSN: 1061-4036 the whole document	1-5, 49-51  6-48, 52
Y	WO 97 20948 A (KOCH JOERN ERLAND) 12 June 1997 (1997-06-12) the whole document	1-52
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Date of the actual completion of the international search

27 April 2000

Date of mailing of the international search report

12/05/2000

Name and mailing address of the ISA

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## INTERNATIONAL SEARCH REPORT

Intern. Patent Application No.

PCT/US 99/21291

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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Y	WO 98 14610 A (PERKIN ELMER CORP) 9 April 1998 (1998-04-09) the whole document	1-52
Y	CHEN ET AL.: "AMPLIFICATION OF CLOSED CIRCULAR DNA IN VITRO" NUCLEIC ACIDS RESEARCH, vol. 26, no. 4, February 1998 (1998-02), pages 1126-1127, XP002136565 the whole document	1-52
A	US 5 714 320 A (KOOL ERIC T) 3 February 1998 (1998-02-03) the whole document	
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Information on patent family members

Internat'l Application No

PCT/US 99/21291

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GB 2332516 A	23-06-1999	NONE	





## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification: <b>C12N 15/10, C12Q 1/68</b>	<b>A2</b>	(11) International Publication Number: <b>WO 00/15779</b>
		(43) International Publication Date: 23 March 2000 (23.03.2000)

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L'invention concerne des réactifs et un procédé permettant d'assurer un clonage moléculaire in vitro de molécules d'acides nucléiques déterminées. Etant entièrement in vitro, le procédé peut être automatisé et étendu selon des modalités qu'il est impossible de mettre en oeuvre avec le clonage moléculaire à base cellulaire. Le procédé consiste à insérer la molécule d'acide nucléique concernée dans un vecteur linéaire, de manière à former un vecteur circulaire dans lequel un brin est continu et l'autre brin est discontinu. Le brin continu est ensuite amplifié selon le modèle du cercle roulant, ce qui permet d'amplifier par la même occasion la molécule d'acide nucléique. L'amplification est rapide et efficace car elle fait intervenir une réaction isothermique unique qui assure la réplication exponentielle des séquences du vecteur. Le procédé peut être automatisé lorsque plusieurs réactions sont conduites simultanément dans une zone de taille réduite. L'acide nucléique amplifié peut être utilisé à toute fin et de façon quelconque dans l'éventail d'utilisation connu de l'acide nucléique cloné ou amplifié, y compris le séquençage, la détermination de sondes, l'analyse de restriction, le sous-clonage, la transcription, l'analyse d'hybridation ou de dénaturation, le complément d'amplification et le stockage pour utilisation ou analyse ultérieure.

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(54) Title: MOLECULAR CLONING USING ROLLING CIRCLE AMPLIFICATION		
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Description

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**MOLECULAR CLONING USING  
ROLLING CIRCLE AMPLIFICATION  
BACKGROUND OF THE INVENTION**

The disclosed invention is generally in the field of molecular cloning and nucleic acid amplification, and specifically involves rolling circle replication of nucleic acid molecules inserted into circular vectors.

DNA molecular cloning is routinely carried out using plasmid, phage, or viral vectors that replicate inside cells. A method, in which individual DNA molecules are cloned in solution by serial dilution and subsequent PCR amplification from tubes containing single molecules has been described (Lukyanov *et al.*, *Nucleic Acid Research* 24:2194-2195 (1996)). A method has also been described for cloning RNA populations derived from single RNA molecules in an immobilized medium (Chetverina and Chetverin, *Nucleic Acids Research* 21:2349-2353 (1993)). While both of these methods allow *in vitro* cloning, neither is practical for high throughput cloning.

Velculescu *et al.*, *Science* 270:484-487 (1995), have described a method for the quantitative cataloguing and comparison of expressed genes in normal, developmental, and disease states. The method, termed serial analysis of gene expression (SAGE), is based in the use of relatively short sequence tags for the unique identification of cDNAs derived from mRNA transcripts. While this method is very powerful, the study of low-abundance mRNAs can require several months of work in order to obtain sufficient sequence information for a complete SAGE analysis of one tissue sample. Thus, there is a need for a method to obtain the sequence of sequence tags more rapidly.

It is therefore an object of the present invention to provide a more efficient method of *in vitro* molecular cloning.

It is also an object of the present invention to provide vectors and kits useful for *in vitro* cloning.

It is also an object of the present invention to provide an automated method molecular cloning.

It is also an object of the present invention to provide a more efficient method of sequential analysis of gene expression.

## BRIEF SUMMARY OF THE INVENTION

Disclosed are reagents and a method for efficient *in vitro* molecular cloning of nucleic acid molecules of interest. Because the method is entirely *in vitro*, it can be automated and scaled-up in ways that are not possible in cell-based molecular cloning. The method involves insertion of a nucleic acid molecule of interest in a linear vector to form a circular vector where one strand is continuous and the other strand is discontinuous. The continuous strand of the circular vector is then amplified by rolling circle replication, amplifying the inserted nucleic acid molecule in the process. The amplification is rapid and efficient since it involves a single, isothermal reaction that replicates the vector sequences exponentially. The amplification process is amenable to automation where multiple reactions are carried out simultaneously in a small area. The amplified nucleic acid can be used for any purpose and in any manner that nucleic acid cloned or amplified by known methods can be used. This includes sequencing, probing, restriction analysis, subcloning, transcription, hybridization or denaturation analysis, further amplified, and storage for future use or analysis.

The insertion reaction involves insertion of a double-stranded nucleic acid molecule into a double-stranded linear vector to produce a double-stranded circular vector. The use of circular vectors facilitates the selection of molecules that have successfully incorporated inserts. The amplification reaction involves rolling circle replication of a single-stranded circular nucleic acid molecule.

A key feature of the method, which facilitates double-stranded insertion followed by single-stranded amplification, is formation of the circular vector in such a way that one of its strands is a closed circular strand (that is, continuous) while the other strand is not a closed circular strand (that is, it has a nick, a gap, an overlap, or is otherwise discontinuous). This feature is most useful, and most effectively accomplished, when, by operation of the method, the closed strand and the open strand are predetermined; that is, when a particular strand of the vector is selectively left discontinuous.

5 With rolling circle replication, amplification takes place not in cycles, but in a continuous, isothermal replication. This makes amplification less complicated and much more consistent in output. A single round of rolling circle replication results in a large amplification of the circular vector, orders  
10 of magnitude greater than a single cycle of PCR replication and other amplification techniques in which each cycle is limited to a doubling of the number of copies of a target sequence.

15 Following amplification, the amplified nucleic acid can be used for any purpose. Numerous methods for the use and manipulation of cloned or isolated nucleic acid are known and can be applied to nucleic acid amplified  
20 in the present method. For example, the nucleic acid can be sequenced, probed, subjected to restriction analysis, subcloned, transcribed, subjected to hybridization or denaturation analysis, further amplified, or stored. Diagnostic methods, such as sequencing and probing for specific sequences,  
25 are preferred.

Libraries of cloned nucleic acids formed by the disclosed method can be screened using any of the methods used for screening conventional libraries. For example, cDNA libraries made using the disclosed method can  
30 be analyzed using conventional screens. Libraries can also be used for *in situ* transcription to generate RNA colonies, which can then be analyzed (*in situ* or in replicas) by appropriate screens, such as aptamer screens or ribozyme activity screens. Libraries can also be screened by *in situ*  
35 translation on array replicas (see, for example, Saris *et al.*, *Nucleic Acids Res.* 10:4831-4843 (1982)). Libraries can also be screened by *in situ* coupled transcription-translation systems, and subsequent catalytic activity assays for  
40 the analysis of mutagenized enzymes. Libraries can be screened and cataloged by sequencing and use of the data for the analysis of cDNA abundancies, which is useful for RNA profiling and serial analysis of gene  
45 expression (SAGE; Velculescu *et al.*, *Science* 270:484-487 (1995)).

#### 30 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a diagram of examples of various forms of linear vectors and the circular vectors, having one continuous strand and one discontinuous  
50 strand, that result upon insertion of a nucleic acid molecule.

5 Figure 2 is a diagram of an example of the disclosed method where the linear vector includes an non-ligatable nick in one of its strands. Upon ligation to form a circular vector, the discontinuous strand is separated from the continuous strand by binding the biotin moiety at the nick to an  
10 immobilized streptavidin moiety.

Figure 3 is a diagram of an example of the disclosed method where the linear vector has an overlap. Upon ligation to form a circular vector (with a Y tail), the discontinuous strand is separated from the continuous strand by ligating one end of the discontinuous strand to an immobilized  
15 nucleic acid probe. This ligation is mediated by hybridization between the single-stranded extension of the discontinuous strand and the probe.

Figure 4 is a diagram of an example of the disclosed method where the linear vector is a linker having sticky ends compatible with sticky ends formed by restriction digestion of PCR primer sequences incorporated at the  
20 ends of PCR amplified DNA. The linker facilitates circularization of the PCR amplified DNA. The linker has one non-ligatable end which, upon ligation, results in a circular molecule with one continuous strand and one discontinuous strand. The discontinuous strand is separated from the continuous strand by binding the biotin moiety at the nick to an immobilized  
25 streptavidin moiety.

#### DETAILED DESCRIPTION OF THE INVENTION

35 Disclosed are reagents and a method for efficient *in vitro* molecular cloning of nucleic acid molecules of interest. Because the method is entirely *in vitro*, it can be automated and scaled-up in ways that are not possible in cell-based molecular cloning. The method involves insertion of a nucleic  
40 acid molecule of interest in a linear vector to form a circular vector where one strand is continuous and the other strand is discontinuous. The continuous strand of the circular vector is then amplified by rolling circle replication, amplifying the inserted nucleic acid molecule in the process.  
45 The amplification is rapid and efficient since it involves a single, isothermal reaction that replicates the vector sequences exponentially. The amplification process is amenable to automation where multiple reactions are carried out simultaneously in a small area. The amplified nucleic acid can be  
50



5 used for any purpose and in any manner that nucleic acid cloned or amplified by known methods can be used. This includes sequencing, probing, restriction analysis, subcloning, transcription, hybridization or denaturation analysis, further amplified, and storage for future use or analysis.

10 5 The insertion reaction involves insertion of a double-stranded nucleic acid molecule into a double-stranded linear vector to produce a double-stranded circular vector. The use of circular vectors facilitates the selection of molecules that have successfully incorporated inserts. The amplification reaction involves rolling circle replication of a single-stranded circular  
15 nucleic acid molecule. In its most useful forms, the disclosed method involves insertion of nucleic acid molecules of interest into a vector and separate amplification of the resulting recombinant vectors to produce separate nucleic acid "colonies," each representing a clonal population of nucleic acid sequences present in founding vector of that "colony."

20 15 A key feature of the method, which facilitates double-stranded insertion followed by single-stranded amplification, is formation of the circular vector in such a way that one of its strands is a closed circular strand (that is, continuous) while the other strand is not a closed circular strand (that is, it has a nick, a gap, an overlap, or is otherwise discontinuous). This  
30 20 feature is most useful, and most effectively accomplished, when, by operation of the method, the closed strand and the open strand are predetermined; that is, when a particular strand of the vector is selectively left discontinuous.

35 With rolling circle replication, amplification takes place not in cycles, but in a continuous, isothermal replication. This makes amplification less  
40 25 complicated and much more consistent in output. A single round of rolling circle replication results in a large amplification of the circular vector, orders of magnitude greater than a single cycle of PCR replication and other amplification techniques in which each cycle is limited to a doubling of the  
45 30 number of copies of a target sequence.

50 The present method is an alternative to traditional molecular cloning involving clonal amplification in cells harnessing the natural nucleic acid replication in, and growth and division of, the cells. The present method has

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5 several advantages over this traditional method. First, it is much more rapid. Traditional molecular cloning usually requires at least twelve hours of cell growth in the best cell-based cloning methods to produce a million copies of a single vector. In contrast, the present method allows production of millions  
10 or billions of copies of a single vector in only 60 to 90 minutes.

Once a clonal culture or colony of cells is grown, there is still the problem of separating the amplified nucleic acid from the cell and all the cellular components. Although numerous methods have been devised over  
15 the years for such purification, they remain both time consuming and ineffective (that is, cellular contaminants remain with the isolated nucleic acid). Generally, the amount of time for the purification and the level of purity obtain from nucleic acid isolation methods is proportional: more time,  
20 more purity; less time, less purity. In contrast, the present method accomplishes clonal amplification in an uncomplicated mix of just a few well-defined components: the vector, one or two types of primers,  
25 nucleotides, and polymerase. The purification of the amplified nucleic acid is correspondingly simplified. Most significantly, the amplification reaction in present method need not result in a complex mixture of nucleic acids as is true of cell-based molecular cloning.

20 The present method also has advantages over cyclic amplification methods such as the polymerase chain reaction (PCR). Rolling circle replication is more rapid and has higher yields than PCR. Significantly, the products of rolling circle replication are tandemly repeated amplicons of double-stranded DNA. These amplicons, if carried as contaminants to any  
35 surface or vessel, are unable to seed new rolling circle replication reactions. In other words, the amplified DNA is non-contaminating because it is a replication dead-end. By contrast, PCR or SDA amplicons are potentially  
40 contaminating.

Following amplification, the amplified nucleic acid can be used for  
45 any purpose. Numerous methods for the use and manipulation of cloned or isolated nucleic acid are known and can be applied to nucleic acid amplified in the present method. For example, the nucleic acid can be sequenced,  
50 probed, subjected to restriction analysis, subcloned, transcribed, subjected to

5 hybridization or denaturation analysis, further amplified, or stored.  
Diagnostic methods, such as sequencing and probing for specific sequences,  
are preferred.

10 The nucleotide sequence of the amplified sequences can be  
5 determined either by conventional means or by primer extension sequencing  
of amplified target sequence. One preferred form of sequencing for use with  
amplified sequences produced with the disclosed method is nanosequencing  
or single-nucleotide extension sequencing. Nanosequencing methods are  
15 described below and by Jalanko *et al.*, *Clinical Chemistry* 38:39-43 (1992);  
Nikiforov *et al.*, *Nucleic Acids Research* 22:4167-4175 (1994); and  
10 Kobayashi *et al.*, *Molecular and Cellular Probes* 9:175-182 (1995).

20 Two forms of sequencing that can be used with the disclosed method  
are described in PCT Application WO 97/20948. One is single nucleotide  
primer extension sequencing involving interrogation of a single nucleotide in  
25 an amplified target sequence by incorporation of a specific and identifiable  
nucleotide based on the identity of the interrogated nucleotide. The other is  
degenerate probe primer extension sequencing involving sequential addition  
of degenerate probes to an interrogation primer hybridized to amplified  
30 target sequences.

20 Libraries of cloned nucleic acids formed by the disclosed method can  
be screened using any of the methods used for screening conventional  
libraries. For example, cDNA libraries made using the disclosed method can  
35 be analyzed using conventional screens. Libraries can also be used for *in situ*  
transcription to generate RNA colonies, which can then be analyzed (*in situ*  
or in replicas) by appropriate screens, such as aptamer screens or  
25 ribozyme activity screens. Libraries can also be screened by *in situ*  
translation on array replicas (see, for example, Saris *et al.*, *Nucleic Acids Res.*  
10:4831-4843 (1982)). Libraries can also be screened by *in situ* coupled  
transcription-translation systems, and subsequent catalytic activity assays for  
45 the analysis of mutagenized enzymes. Libraries can be screened and  
30 cataloged by sequencing and use of the data for the analysis of cDNA  
abundancies, which is useful for RNA profiling and serial analysis of gene  
expression (SAGE; Velculescu *et al.*, *Science* 270:484-487 (1995)).  
50

5 One embodiment of the disclosed method is a method of isolating  
and amplifying a nucleic acid molecule, where the method involves:

10 (a) ligating a nucleic acid molecule into a linear vector to form a  
circular vector including the vector and the nucleic acid molecule, where the  
5 linear vector is a double-stranded linear nucleic acid including two nucleic  
acid strands, where the second strand of the circular vector is discontinuous,  
and where the first strand in the circular vector is a closed circular strand,  
15 and

(b) amplifying the first strand by rolling circle replication to form  
10 tandem sequence DNA, where the amplification results in amplification of  
the nucleic acid molecule in the first strand.

20 The method can be practiced and expanded in several ways. For  
example, the second strand of the linear vector can contain at least one nick,  
where the nick cannot be ligated. The linear vector can be designed such that  
25 either the 5' or the 3' end of the second strand of the linear vector cannot be  
ligated. The linear vector can be designed such that the second strand of the  
linear vector contains at least one gap or overlap. The method can be  
extended to include, following ligation and prior to amplification, separation  
30 of the first strand from the second strand. The second strand of the vector  
can include an affinity tag. In this case, the first strand can be separated from  
20 the second strand by binding the affinity tag to a substrate, denaturing the  
first and second strands prior to, simultaneous with, or following binding,  
35 and separating the first strand from the substrate.

The second strand of the linear vector can also be designed to contain  
25 at least one overlap, where part of the overlapping portions of the second  
strand are complementary, and where the 3' end of the overlap extends  
40 beyond the part of the overlapping portions that are complementary. In this  
case, the first strand can be separated from the second strand by ligating one  
end of the second strand to a nucleic acid molecule coupled to a substrate,  
45 30 denaturing the first and second strands following ligation of the second  
strand, and separating the first strand from the substrate.

The method can also be practiced such that step (a) involves ligating  
50 a plurality of nucleic acid molecules into a plurality of linear vectors in a

5 single reaction to form a plurality of circular vectors, each circular vector  
containing at least one nick, gap, or overlap in the second strand, such that  
step (b) involves amplifying the first strand of the plurality of circular  
10 vectors, and such that, prior to amplification, the ligation reaction is divided  
5 to produce a plurality of separate amplification reactions. The method can be  
extended to include making a replica of the amplification reactions. The  
replica of the amplification reactions can be made by contacting the  
15 amplification reactions with a surface to which nucleic acids can bind. The  
replica of the amplification reactions can also be made by transferring part of  
10 each amplification reaction to form a replica amplification reaction.

20 In the method, the ligation reaction can be divided by spreading the  
ligation reaction onto a surface to form a spread, where the separate  
amplification reactions are the locations of circular vectors on the surface  
after spreading. In this case, a replica of the amplification reactions can be  
25 made by contacting the spread with a second surface to which nucleic acids  
can bind.

30 Any number or all of the amplification reactions can be ordered as an  
array of reaction droplets or in an array of reaction vessels. In this case,  
following amplification, all or part of the contents of any number or all the  
20 individual reaction droplets or reaction vessels are transferred by one to one  
mapping to a new set of reaction droplets or reaction vessels.

35 The method can be further extended by, following amplification,  
determining the presence of amplified nucleic acid in the amplification  
reactions, and transferring all or a part of the contents of the amplification  
25 reactions containing amplified nucleic acid reaction to a new set of reaction  
droplets or reaction vessels.

40 Replicas of the amplification reactions can be made by contacting the  
amplification reactions with a surface treated with an affinity target capable  
of binding an affinity tag, where the amplified nucleic include affinity tags  
45 incorporated during amplification, such that a portion of each amplification  
30 reaction is transferred to the surface. The affinity tag is preferably biotin and  
the affinity target is preferably streptavidin. The affinity tag is also  
50 preferably a reactive moiety and the affinity target is preferably a

5 corresponding reactive moiety, such that a chemical reaction between the  
affinity tag and the affinity target results in the amplified nucleic acid being  
covalently coupled to the surface. In this case, it is preferred that the affinity  
target is phenylene diisothiocyanate, disuccinimidylcarbonate,  
10 disuccinimidylsuccinate or dimethylsuberimide and the affinity tag is a  
reactive amine.

A replica of the amplification reactions can also be made by  
transferring part of each amplification reaction to form a replica  
15 amplification reaction. Following amplification, all or part of the contents of  
any number or all of the reaction droplets or reaction vessels can be  
transferred and combined to create one or more sets of pooled reactions. The  
20 amplification reactions can also be arranged on the surface of a substrate.  
Preferred substrates include acrylamide, cellulose, nitrocellulose,  
polystyrene, polyethylene vinyl acetate, polypropylene, polymethacrylate,  
15 polyethylene, polyethylene oxide, glass, polysilicates, polycarbonates, tetlon,  
fluorocarbons, nylon, silicon rubber, polyanhydrides, polyglycolic acid,  
polylactic acid, polyorthoesters, polypropylfumarate, collagen,  
glycosaminoglycans, polyamino acids, chemical resistant metals, or  
30 corrosion resistant metals.

20 The ligation reactions can also be diluted prior to division of the  
ligation reaction into amplification reactions such that, on average, each  
amplification reaction contains a single circular vector. A sample of each  
35 amplification reaction can also be collected. Nucleic acid molecules in the  
amplification reactions or in the collected samples can also be detected or  
sequenced.

40 In the disclosed method, rolling circle replication can be primed by  
the second strand on the circular vector or by a rolling circle replication  
primer. The tandem sequence DNA formed after amplification can itself be  
amplified by strand displacement replication to form secondary tandem  
45 sequence DNA. This secondary tandem sequence DNA can also be  
amplified by strand displacement replication to form tertiary tandem  
sequence DNA. Strand displacement replication of the tandem sequence can  
50 be primed by a strand displacement primer.

5 The method can also include detection of one or more amplified nucleic acid molecules in one or more of the amplification reactions. In a preferred embodiment, the nucleic acid molecules can be derived from cDNA generated by suppression subtractive hybridization. In another  
10 5 preferred embodiment, the plurality of nucleic acid molecules can be all derived from the same source.

Detection can be accomplished by, following amplification, creating a replica of the amplification reactions, contacting the amplification reactions with a first set of labeled nucleic acid probes and the replica amplification  
15 10 reactions with a second set of labeled nucleic acid probes, and comparing the pattern of hybridization of the first set of probes to the pattern of hybridization of the second set of probes, where differences in the patterns of hybridization indicate differences in the probe sets. Following detection  
20 amplification reactions that hybridize to the first set of probes but not to the second set of probes, amplification reactions that hybridize to the second set  
25 15 of probes but not to the first set of probes, amplification reactions that hybridize to the both sets of probes, or amplification reactions that do not hybridize to either set of probes can be selected for isolation or further analysis.

30 20 Another embodiment of the disclosed method is an *in vitro* method of cloning nucleic acid molecules, where the method involves

35 (a) dividing a nucleic acid sample to produce a plurality of separate amplification reactions,

(b) amplifying nucleic acid molecules in the amplification reactions,

25 (c) making a replica of the amplification reactions,

40 (d) testing nucleic acid molecules in either the amplification reactions or the replica amplification reactions to identify nucleic acid molecules of interest, and

45 30 (e) retrieving the identified nucleic acid molecules of interest from the corresponding amplification reactions or replica amplification reactions that were not tested.

In this embodiment, the nucleic acid sample can be divided by spreading the sample onto a surface to form a spread, such that the separate

5 amplification reactions are the locations of circular vectors on the surface after spreading. The replica of the amplification reactions can be made by contacting the spread with a second surface to which nucleic acids can bind.

Another embodiment of the disclosed method is a method of isolating

10 5 and amplifying nucleic acid molecules, where the method involves

(a) ligating a plurality of nucleic acid molecules into a plurality of linear vectors in a single reaction to form a plurality of circular vectors, each circular vector including a vector and a nucleic acid molecule, where the linear vectors are double-stranded linear nucleic acid comprising two nucleic acid strands, where the circular vectors each contain at least one nick, gap, or overlap in the second strand, and where the first strand in each circular vector is a closed circular strand,

(b) separating the first strands from the second strands,

(c) diluting and dividing the first strands to produce a plurality of separate amplification reactions that, on average, each contain a single circular vector,

(d) amplifying the first strands of the plurality of circular vectors by rolling circle replication to form tandem sequence DNA, where the amplification results in amplification of the nucleic acid molecules in the first strands.

The tandem sequence DNA formed after amplification can itself be amplified by strand displacement replication to form secondary tandem sequence DNA. This secondary tandem sequence DNA can also be amplified by strand displacement replication to form tertiary tandem sequence DNA.

Another embodiment of the disclosed method is a method of isolating and amplifying a nucleic acid molecule, where the method involves

(a) ligating a nucleic acid molecule into a linear vector to form a circular vector comprising the vector and the nucleic acid molecule, where the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, where the circular vector contains at least one nick in the second strand, and where the first strand in the circular vector is a closed circular strand,



(b) amplifying the first strand, where the amplification results in amplification of the nucleic acid molecule in the first strand.

Also disclosed is a kit for isolating and amplifying nucleic acid molecules, where the kit includes

(a) a linear vector where the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, and where

(1) the linear vector contains at least one nick, where the nick cannot be ligated,

(2) either the 5' or the 3' end of the second strand of the linear vector cannot be ligated,

(3) the second strand of the linear vector contains at least one gap,

(4) the second strand of the linear vector contains at least one overlap, or

(5) any combination of (1), (2), (3) or (4);

(b) a rolling circle replication primer, where the rolling circle replication primer is complementary to a portion of the first strand of the linear vector; and

(c) a strand displacement primer, where the strand displacement primer matches a portion of the first strand of the linear vector.

Also disclosed is a linear vector where the linear vector is a double-stranded linear nucleic acid made up of two nucleic acid strands, where the second strand of the linear vector contains an affinity tag, and where

(1) the linear vector contains at least one nick, where the nick cannot be ligated,

(2) either the 5' or the 3' end of the second strand of the linear vector cannot be ligated,

(3) the second strand of the linear vector contains at least one gap,

(4) the second strand of the linear vector contains at least one overlap, or

(5) any combination of (1), (2), (3) or (4).

Also disclosed is a linear vector where the linear vector is a double-stranded linear nucleic acid made up of two nucleic acid strands, where the second strand of the linear vector contains at least one overlap, part of the overlapping portions of the second strand are complementary, and the 3' end of the overlap extends beyond the part of the overlapping portions that are complementary.

#### I. Materials

The disclosed method makes use of linear vectors in which nucleic acid molecules of interest can be inserted to form circular vectors. The circular vectors contain one continuous strand and one discontinuous strand. The discontinuous strand may include an affinity tag which, by interaction with an affinity substrate, can facilitate separation of the continuous strand from the discontinuous strand. The continuous strand of the circular vector is amplified by rolling circle replication to form tandem sequence DNA (TS-DNA). Rolling circle replication is primed by a rolling circle replication primer complementary to a sequence in the continuous strand. The tandem sequence DNA itself may be amplified by strand displacement replication, to form secondary tandem sequence DNA, using strand displacement primers (complementary to a sequence in the tandem sequence DNA). The secondary tandem sequence DNA may also be amplified by strand displacement replication, to form tertiary tandem sequence DNA, using strand displacement primers or the rolling circle replication primers (complementary to a sequence in the secondary tandem sequence DNA). Multiple amplification reactions can be carried out in parallel, preferably in arrays or as spreads of diluted vectors on surfaces or embedded in agarose. The resulting "colonies" of amplified DNA represent molecular clones of the progenitor circular vectors with an inserted nucleic acid molecule. Collectively, such colonies form a library of cloned nucleic acid molecules that can be replica plated or arrayed, stored, and screened. These materials are described in detail below.

##### A. Nucleic Acid Molecules

The disclosed method can be used to clone or amplify any nucleic acid molecule of interest. The nucleic acid molecules can come from any

5 source such as a cellular or tissue nucleic acid sample, a subclone of a  
previously cloned fragment, mRNA, chemically synthesized nucleic acid,  
genomic nucleic acid samples, nucleic acid molecules obtained from nucleic  
acid libraries, specific nucleic acid molecules, and mixtures of nucleic acid  
10 molecules. The disclosed method is particularly suited to producing libraries  
of cloned nucleic acid molecules starting with a complex mixture of nucleic  
acid molecules to be represented in the library. For example, cDNA can be  
produced from all of the mRNA in a cellular sample and used to make a  
cDNA library, or a library of genomic DNA can be produced from a  
15 genomic nucleic acid sample.

In the method, the nucleic acid molecule is inserted into a double-  
20 stranded linear vector. Preferably the insertion is accomplished by ligation,  
although any suitable coupling mechanism can also be used. Thus, the only  
requirement for nucleic acids molecules to be used in the disclosed method is  
25 that they can be coupled to the ends of a double-stranded nucleic acid  
molecule (that is, the linear vector). Single-stranded nucleic acid molecules,  
such as RNA, can be used by converting the molecule to be double-stranded.  
In the case of RNA molecules, this can be accomplished, for example, by  
producing a cDNA molecule of the RNA. Numerous methods are known for  
30 preparing and inserting nucleic acid molecules into vectors and any of these  
can be used to prepare nucleic acid molecules for use in the disclosed method  
(see, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory  
Manual*, 2nd Edition (Cold Spring Harbor Laboratory Press, Cold Spring  
35 Harbor, N.Y., 1989)). Preferably, the nucleic acid molecule is prepared by  
generating sticky ends to facilitate insertion in the linear vector. This can be  
25 accomplished, for example by cleaving a nucleic acid molecule of interest, or  
a nucleic acid sample, with a restriction enzyme, or by adding linkers to the  
ends of nucleic acid molecules of interest that have, or can be processed to  
have sticky ends. One or both of the ends of the nucleic acid molecule can  
also be left blunt ended. The two ends of nucleic acid molecules to be used  
30 in the disclosed method can also be made different to allow directional  
insertion. For example, the two ends can have different sticky ends, or have  
one sticky end and one blunt end.

**B. Linear Vectors**

Linear vectors for use in the disclosed method are double-stranded nucleic acid molecules that can be circularized when its ends are coupled to a nucleic acid molecule. The characteristics of the linear vector are limited only by the requirements for the circular vector that results upon insertion of the nucleic acid molecule. Thus, the linear vector is designed such that, when the nucleic acid molecule is inserted and the linear vector is circularized, the resulting circular vector has one continuous, circular strand and one discontinuous strand.

The use of the term vector is not meant to indicate that the linear vector is required to have any characteristics beyond these, such as promoters, selectable markers, origins of replication, and other features present on traditional vectors for cloning in cells. However, the linear vector may contain these or any other features that do not interfere with the disclosed method. Such additional characteristics may be useful, for example, to allow transfer of the vector to cells to obtain expression, or to allow in vitro expression. Thus, the linear vector can be as simple as a short linker that facilitates circularization of a nucleic acid molecule of interest.

The linear vector is a double-stranded nucleic acid molecule where one of the strands will become part of the continuous strand of the circular vector and the other strand will become part of the discontinuous strand of the circular vector. For identification, the strand of the linear vector which will become part of the continuous strand of the circular vector is referred to as the first strand of the linear vector, and the strand of the linear vector which will become part of the discontinuous strand of the circular vector is referred to as the second strand of the linear vector. The first strand of a linear vector includes a sequence complementary to a rolling circle replication primer. This sequence is referred to as the primer complement portion of the linear vector. This facilitates amplification of the circular vector formed from the linear vector by rolling circle replication primed by the rolling circle replication primer. A separate primer complement portion is not required if the second strand of the circular vector is to serve as the rolling circle replication primer. It is preferred that the primer complement

5 portion of the linear vector is near the 5' end of the first strand of the linear vector.

10 The production of a circular vector in the disclosed method is facilitated by giving the first strand and the second strand of the linear vector different characteristics. Although the linear vector is referred to as having 5 two strands, each of these "strands" may be made up of more than one linear nucleic acid strands. That is, the first strand of the linear nucleic acid molecule may be made up of multiple nucleic acid molecules lying end to 15 end and hybridized to the second strand. Similarly, the second strand of the linear nucleic acid molecule may be made up of multiple strands hybridized to the first strand. The use of the terms first "strand" and second "strand" are used as a convenience to refer to all of the physical nucleic acid strands that 20 make up one side of the linear vector. The relationship of the physical strands in the linear vector to the collective first and second strands can be seen in Figure 1. The first strand of the linear vector is preferably composed 25 of one strand. The second strand is preferably composed of more than one strand, and most preferably composed of two strands.

30 All of the ends present in the first strand of the linear vector, including internal ends, if present, should be ligatable. Ligatable ends are ends that can be ligated to compatible ends by ligase, or which can otherwise 35 be coupled to compatible ends. Preferred ligatable ends are nucleotides having a 3' hydroxyl or a 5' phosphate. Internal ends are ligatable only if compatible ends are adjacent. For example, a nick with a 3' hydroxyl on one end and a 5' phosphate on the other end is a ligatable nick and the ends are 25 ligatable. Nick has its usual meaning. Specifically, a nick is a break in a strand hybridized to another strand where there are no unpaired nucleotides in the other strand opposite the nick. 40

45 To result in a discontinuous second strand in the circular vector, the second strand of the linear vector should contain at least one non-ligatable end or at least one gap or overlap. Non-ligatable ends are ends that cannot be 30 ligated to compatible ends by ligase, or which cannot otherwise be coupled to compatible ends. Preferred non-ligatable ends are nucleotides having a blocking group at the 3' or 5' position. For example, the second strand of the 50

linear vector can include a 3'-terminal or 5'-terminal biotin residue (either at the end of a continuous second strand or at a nick in a discontinuous second strand). This residue renders the terminus non-ligatable, causing all vectors to contain a nick after cloning of inserts by ligation. This biotin residue can then used as a handle to remove the second strand of the circularized vector, generating single-stranded circles for amplification. Thus, the biotin is both a blocking group and an affinity tag.

Internal ends are also non-ligatable if, for example, compatible ends are not adjacent. For example, a nick with a 3' hydroxyl on both ends is an unligatable nick and the ends are unligatable. A nick with a blocking group on one of the ends is also an unligatable nick and the end with the blocking group is an unligatable end. Both gaps and overlaps is not ligatable even if the ends would otherwise be compatible since the ends are not close enough to be coupled. Gap has its usual meaning. Specifically, a gap is a break in a strand hybridized to another strand where there is at least one nucleotide on the other strand opposite the gap that is unpaired. A gap can also occur at the end of the linear vector in that a nucleic acid molecule, when hybridized to sticky ends of the linear vector, can fail to extend to the end of one of the strands of the linear vector.

An overlap occurs where the adjacent ends of two strands hybridized adjacent to each other on another strand extend beyond the region of hybridization. A preferred form of overlap is where the two overlapping strands hybridize to each other in the overlapping region. This type of overlap in a linear vector produces a Y shaped molecule such as the one illustrated in Figure 1 and in Figure 3.

The second strand of the linear vector may contain multiple nicks, gaps, and overlaps in any combination. Any number of such nicks may be ligatable or non-ligatable. All that is required is at least one feature that prevents the second strand of the circular vector from being continuous following insertion of the nucleic acid molecule. For this purpose, a single non-ligatable end or other non-ligatable feature is all that is required. The first strand of the linear vector contain multiple nicks so long as they are all

ligatable; that is, so long as the first strand of the circular vector will be continuous following insertion of the nucleic acid molecule.

The second strand of the linear vector can also contain one or more affinity tags to facilitate separation of the first and second strands of the circular vector formed from the linear vector. It is preferred that linear vectors include either pre-formed sticky ends or one or more restriction enzymes sites near the ends of the linear vector to facilitate insertion of nucleic acid molecules into the vectors. Multiple cloning sites (MCS) are particularly preferred. Such MCSs facilitate both insertion of a nucleic acid molecule of interest into linear vectors and removal of the nucleic acid molecule from the amplified nucleic acid. It is preferred that the ends of the linear vector, when ready for ligation, do not contain compatible ends that can be ligated. This will prevent the circularization of linear vectors in the absence of insertion of a nucleic acid molecule.

#### C. Circular Vectors

A circular vector is a double-stranded circular nucleic acid molecule that is a combination of a linear vector and one or more inserted nucleic acid molecules. One of the strands of the circular vector, termed the first strand, is continuous. That is, the first strand of the circular vector is a closed circular nucleic acid strand. The other strand of the circular vector, termed the second strand, is discontinuous. That is, the second strand of the circular vector is not a closed circular nucleic acid strand. The second strand can include, for example, nicks, gaps, and overlaps. The discontinuity of the second strand allows the separation of the first and second strands following denaturation. The second strand of the circular vector can also contain one or more affinity tags to facilitate separation of the first and second strands of the circular vector.

The first strand of a circular vector includes a sequence complementary to a rolling circle replication primer. This sequence is referred to as the primer complement portion of the circular vector. This facilitates amplification of the circular vector by rolling circle replication primed by the rolling circle replication primer. A separate primer

complement portion is not required if the second strand of the circular vector is to serve as the rolling circle replication primer.

#### **D. Affinity Tags**

An affinity tag is a molecule that interacts specifically with a particular molecule or moiety. The molecule or moiety that interacts specifically with an affinity tag is referred to herein as an affinity target. Together, an affinity tag and affinity target make up a binding pair. Either member of a binding pair can be used as an affinity tag and either member can be used as an affinity target. An affinity tag is the member of the binding pair coupled to the linear or circular vector. A preferred binding pair is biotin and streptavidin. It is to be understood that the term affinity target refers to both separate molecules and to portions of molecules, such as an epitope of a protein, that interacts specifically with an affinity tag. Antibodies, either member of a receptor/ligand pair, and other molecules with specific binding affinities are examples of affinity tags, useful as the affinity portion of a reporter binding molecule. By coupling an affinity tag to the second strand of a linear vector, binding of the affinity tag to its affinity target allows separation of the first and second strands of the circular vector. An affinity tag that interacts specifically with a particular affinity target is said to be specific for that affinity target. For example, an affinity tag which is an antibody that binds to a particular antigen is said to be specific for that antigen. The antigen is the affinity target. Complementary nucleotide sequences can be used as binding pairs. An example of this is illustrated with the immobilization of Y shaped circular vector in Figure 3.

#### **E. Affinity Substrates**

Affinity substrates are solid-state substrates or supports to which affinity targets have been coupled. Generally, an affinity substrate is used to facilitate separation of first and second strands of circular vectors by immobilizing the second strands of circular vectors to a solid-state substrate or support via an affinity tag. Solid-state substrates for use in affinity substrates can include any solid material to which affinity targets can be coupled. This includes materials such as acrylamide, cellulose, nitrocellulose, polystyrene, polyethylene vinyl acetate, polypropylene,



5 polymethacrylate, polyethylene, polyethylene oxide, glass, polysilicates,  
polycarbonates, teflon, fluorocarbons, nylon, silicon rubber, polyanhydrides,  
polyglycolic acid, polylactic acid, polyorthoesters, polypropylfumerate,  
collagen, glycosaminoglycans, polyamino acids, chemical resistant metals,  
10 and corrosion resistant metals. Solid-state substrates can have any useful  
form including thin films or membranes, beads, bottles, dishes, fibers, woven  
fibers, shaped polymers, particles and microparticles. A preferred form for a  
solid-state substrate is a bead or surface.

15 Affinity targets immobilized on a solid-state substrate allow capture  
of the second strand of circular vectors on a affinity substrate. Such capture  
provides a convenient means of separating the seconds strands from the first  
strands of circular vectors (which are to be amplified).

20 Methods for immobilizing proteins, such as antibodies, to solid-state  
substrates are well established. Immobilization can be accomplished by  
attachment, for example, to aminated surfaces, carboxylated surfaces or  
hydroxylated surfaces using standard immobilization chemistries. Examples  
25 of attachment agents are cyanogen bromide, succinimide, aldehydes, tosyl  
chloride, avidin-biotin, photocrosslinkable agents, epoxides and maleimides.  
A preferred attachment agent is glutaraldehyde. These and other attachment  
agents, as well as methods for their use in attachment, are described in  
30 *Protein immobilization: fundamentals and applications*, Richard F. Taylor,  
ed. (M. Dekker, New York, 1991), Johnstone and Thorpe, *Immunochemistry  
In Practice* (Blackwell Scientific Publications, Oxford, England, 1987) pages  
209-216 and 241-242, and *Immobilized Affinity Ligands*, Craig T.

35 Hermanson *et al.*, eds. (Academic Press, New York, 1992). Proteins, and  
other affinity targets having free amino groups, can be attached to a substrate  
by chemically cross-linking a free amino group on the protein to reactive  
side groups present within the solid-state substrate. For example, proteins  
may be chemically cross-linked to a substrate that contains free amino or  
40 carboxyl groups using glutaraldehyde or carbodiimides as cross-linker  
agents. In this method, aqueous solutions containing free proteins are  
incubated with the solid-state substrate in the presence of glutaraldehyde or  
carbodiimide. For crosslinking with glutaraldehyde the reactants can be  
50

incubated with 2% glutaraldehyde by volume in a buffered solution such as 0.1 M sodium cacodylate at pH 7.4. Other standard immobilization chemistries are known by those of skill in the art.

Methods for immobilization of oligonucleotides to solid-state substrates are well established. Oligonucleotides, including affinity targets, can be coupled to substrates using established coupling methods. For example, suitable attachment methods are described by Pease *et al.*, *Proc. Natl. Acad. Sci. USA* 91(11):5022-5026 (1994), and Khrapko *et al.*, *Mol Biol (Mosk) (USSR)* 25:718-730 (1991). A method for immobilization of 3'-amine oligonucleotides on casein-coated slides is described by Stimpson *et al.*, *Proc. Natl. Acad. Sci. USA* 92:6379-6383 (1995). A preferred method of attaching oligonucleotides to solid-state substrates is described by Guo *et al.*, *Nucleic Acids Res.* 22:5456-5465 (1994).

#### F. Rolling Circle Replication Primer

A rolling circle replication primer (RCRP) is an oligonucleotide having sequence complementary to the primer complement portion of the first strand of a circular vector. This sequence is referred to as the complementary portion of the RCRP. The complementary portion of a RCRP and the cognate primer complement portion can have any desired sequence so long as they are complementary to each other. In general, the sequence of the RCRP can be chosen such that it is not significantly complementary to any other portion of the circular vector. The complementary portion of a rolling circle replication primer can be any length that supports specific and stable hybridization between the primer and the primer complement portion. Generally this is 10 to 35 nucleotides long, but is preferably 16 to 20 nucleotides long. A separate rolling circle replication primer is not required if the second strand of the circular vector is to serve as the rolling circle replication primer. In this case, the second strand of the circular vector can be referred to as a rolling circle replication primer.

It is preferred that rolling circle replication primers also contain additional sequence at the 5' end of the RCRP that is not complementary to any part of the circular vector. This sequence is referred to as the non-

5 complementary portion of the RCRP. The non-complementary portion of  
the RCRP, if present, serves to facilitate strand displacement during DNA  
replication. The non-complementary portion of a RCRP may be any length,  
but is generally 1 to 100 nucleotides long, and preferably 4 to 8 nucleotides  
10 long. The rolling circle replication primer may also include modified  
nucleotides to make it resistant to exonuclease digestion. For example, the  
primer can have three or four phosphorothioate linkages between nucleotides  
at the 5' end of the primer. Such nuclease resistant primers allow selective  
15 degradation of excess unligated linear vector that might otherwise interfere  
with hybridization of probes and primers to the amplified nucleic acid. A  
rolling circle replication primer can be used as the tertiary strand  
displacement primer in strand displacement cascade amplification.  
20

#### G. Strand Displacement Primers

Primers used for strand displacement replication are referred to herein  
15 as strand displacement primers. One form of strand displacement primer,  
referred to herein as a secondary strand displacement primer, is an  
oligonucleotide having sequence matching part of the sequence of the first  
strand of a circular vector. This sequence is referred to as the matching  
30 portion of the strand displacement primer. This matching portion of a  
secondary strand displacement primer is complementary to sequences in  
tandem sequence DNA (TS-DNA). The matching portion of a secondary  
strand displacement primer may be complementary to any sequence in TS-  
35 DNA. However, it is preferred that it not be complementary TS-DNA  
sequence matching either the rolling circle replication primer or a tertiary  
strand displacement primer, if one is being used. This prevents hybridization  
40 of the primers to each other. The matching portion of a strand displacement  
primer may be complementary to all or a portion of the inserted nucleic acid  
molecule, although this is not preferred. The matching portion of a strand  
displacement primer can be any length that supports specific and stable  
45 hybridization between the primer and its complement. Generally this is 12 to  
30 35 nucleotides long, but is preferably 18 to 25 nucleotides long. It is  
preferred that the matching portion of the circular vector is near the 3' end of  
the first strand of the circular vector.  
50

5 It is preferred that secondary strand displacement primers also  
contain additional sequence at their 5' end that does not match any part of the  
first strand of the circular vector. This sequence is referred to as the non-  
10 matching portion of the strand displacement primer. The non-matching  
5 portion of the strand displacement primer, if present, serves to facilitate  
strand displacement during DNA replication. The non-matching portion of a  
strand displacement primer may be any length, but is generally 1 to 100  
15 nucleotides long, and preferably 4 to 8 nucleotides long.

Another form of strand displacement primer, referred to herein as a  
10 tertiary strand displacement primer, is an oligonucleotide having sequence  
complementary to part of the sequence of the first strand of the circular  
20 vector. This sequence is referred to as the complementary portion of the  
tertiary strand displacement primer. This complementary portion of the  
tertiary strand displacement primer matches sequences in TS-DNA. The  
15 complementary portion of a tertiary strand displacement primer may be  
complementary to any sequence in the first strand of the circular vector.  
However, it is preferred that it not be complementary to a sequence matching  
the strand displacement primer. This prevents hybridization of the primers to  
30 each other. The complementary portion of a tertiary strand displacement  
20 primer can be any length that supports specific and stable hybridization  
between the primer and its complement. Generally this is 12 to 35  
nucleotides long, but is preferably 18 to 25 nucleotides long. It is preferred  
35 that tertiary strand displacement primers also contain additional sequence at  
their 5' end that is not complementary to any part of the first strand of the  
25 circular vector. This sequence is referred to as the non-complementary  
portion of the tertiary strand displacement primer. The non-complementary  
40 portion of the tertiary strand displacement primer, if present, serves to  
facilitate strand displacement during DNA replication. The non-  
complementary portion of a tertiary strand displacement primer may be any  
45 30 length, but is generally 1 to 100 nucleotides long, and preferably 4 to 8  
nucleotides long. A rolling circle replication primer is a preferred form of  
tertiary strand displacement primer. It is preferred that the complementary

5 portion of the circular vector is near the 5' end of the first strand of the circular vector.

Strand displacement primers may also include modified nucleotides to make them resistant to exonuclease digestion. For example, the primer  
10 5 can have three or four phosphorothioate linkages between nucleotides at the 5' end of the primer. Such nuclease resistant primers allow selective degradation of excess unligated linear vectors that might otherwise interfere with hybridization of probes and primers to the amplified nucleic acid.  
15 Strand displacement primers can be used for strand displacement replication and strand displacement cascade amplification, both described below.

## II. Synthesis of Oligonucleotides

20 Linear vectors, rolling circle replication primers, strand displacement primers, and any other oligonucleotides can be synthesized using established oligonucleotide synthesis methods. Methods to produce or synthesize  
25 oligonucleotides are well known in the art. Such methods can range from standard enzymatic digestion followed by nucleotide fragment isolation (see for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Edition (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989) Chapters 5, 6) to purely synthetic methods, for example, by the  
30 cyanoethyl phosphoramidite method using a Milligen or Beckman System I Plus DNA synthesizer (for example, Model 8700 automated synthesizer of Milligen-Bioscience, Burlington, MA or ABI Model 380B). Synthetic  
35 methods useful for making oligonucleotides are also described by Ikuta *et al.*, *Ann. Rev. Biochem.* 53:323-356 (1984), (phosphotriester and phosphite-triester methods), and Narang *et al.*, *Methods Enzymol.* 65:610-620 (1980),  
40 (phosphotriester method). Protein nucleic acid molecules can be made using known methods such as those described by Nielsen *et al.*, *Bioconjug. Chem.* 5:3-7 (1994).

Many of the oligonucleotides described herein are designed to be  
45 30 complementary to certain portions of other oligonucleotides or nucleic acids such that stable hybrids can be formed between them. The stability of these hybrids can be calculated using known methods such as those described in Lesnick and Freier, *Biochemistry* 34:10807-10815 (1995), McGraw *et al.*,  
50

5 *Biotechniques* 8:674-678 (1990), and Rychlik *et al.*, *Nucleic Acids Res.*  
18:6409-6412 (1990).

#### I. DNA ligases

Any DNA ligase is suitable for use in the disclosed method.

- 10 5 Preferred ligases are those that preferentially form phosphodiester bonds at  
nicks in double-stranded DNA. That is, ligases that fail to ligate the free  
ends of single-stranded DNA at a significant rate are preferred.
- 15 Thermostable ligases are especially preferred. Many suitable ligases are  
known, such as T4 DNA ligase (Davis *et al.*, *Advanced Bacterial Genetics -*  
20 *A Manual for Genetic Engineering* (Cold Spring Harbor Laboratory, Cold  
Spring Harbor, N.Y., 1980)), *E. coli* DNA ligase (Panasenko *et al.*, *J. Biol.*  
*Chem.* 253:4590-4592 (1978)), AMPLIGASE® (Kalin *et al.*, *Mutat. Res.*,  
283(2):119-123 (1992); Winn-Deen *et al.*, *Mol Cell Probes* (England)  
7(3):179-186 (1993)), Taq DNA ligase (Barany, *Proc. Natl. Acad. Sci. USA*  
25 88:189-193 (1991), *Thermus thermophilus* DNA ligase (Abbott  
Laboratories), *Thermus scotoductus* DNA ligase and *Rhodothermus marinus*  
DNA ligase (Thorbjarnardottir *et al.*, *Gene* 151:177-180 (1995)). T4 DNA  
ligase is preferred for ligations involving RNA target sequences due to its  
30 ability to ligate DNA ends involved in DNA:RNA hybrids (Hsuih *et al.*,  
20 *Quantitative detection of HCV RNA using novel ligation-dependent*  
*polymerase chain reaction*, American Association for the Study of Liver  
Diseases (Chicago, IL, November 3-7, 1995)).

#### J. DNA polymerases

- 35 DNA polymerases useful in rolling circle replication must perform
- 25 rolling circle replication of primed single-stranded circles. Such  
polymerases are referred to herein as rolling circle DNA polymerases. For  
40 rolling circle replication, it is preferred that a DNA polymerase be capable of  
displacing the strand complementary to the template strand, termed strand  
displacement, and lack a 5' to 3' exonuclease activity. Strand displacement is  
45 necessary to result in synthesis of multiple tandem copies of the circular  
vector. A 5' to 3' exonuclease activity, if present, might result in the  
destruction of the synthesized strand. It is also preferred that DNA  
50 polymerases for use in the disclosed method are highly processive. The

suitability of a DNA polymerase for use in the disclosed method can be readily determined by assessing its ability to carry out rolling circle replication. Preferred rolling circle DNA polymerases are bacteriophage  $\phi$ 29 DNA polymerase (U.S. Patent Nos. 5,198,543 and 5,001,050 to Blanco *et al.*), phage M2 DNA polymerase (Matsumoto *et al.*, *Gene* 84:247 (1989)), phage  $\phi$ PRD1 DNA polymerase (Jung *et al.*, *Proc. Natl. Acad. Sci. USA* 84:8287 (1987)), VENT® DNA polymerase (Kong *et al.*, *J. Biol. Chem.* 268:1965-1975 (1993)), Klenow fragment of DNA polymerase I (Jacobsen *et al.*, *Eur. J. Biochem.* 45:623-627 (1974)), T5 DNA polymerase (Chatterjee *et al.*, *Gene* 97:13-19 (1991)), PRD1 DNA polymerase (Zhu and Ito, *Biochim. Biophys. Acta.* 1219:267-276 (1994)), modified T7 DNA polymerase (Tabor and Richardson, *J. Biol. Chem.* 262:15330-15333 (1987); Tabor and Richardson, *J. Biol. Chem.* 264:6447-6458 (1989); Sequenase™ (U.S. Biochemicals)), and T4 DNA polymerase holoenzyme (Kaboord and Benkovic, *Curr. Biol.* 5:149-157 (1995)).  $\phi$ 29 DNA polymerase is most preferred. Rolling circle DNA polymerases are also generally useful for strand displacement replication.

Strand displacement can be facilitated through the use of a strand displacement factor, such as helicase. It is considered that any DNA polymerase that can perform rolling circle replication in the presence of a strand displacement factor is suitable for use in the disclosed method, even if the DNA polymerase does not perform rolling circle replication in the absence of such a factor. Strand displacement factors useful in RCA include BMRF1 polymerase accessory subunit (Tsurumi *et al.*, *J. Virology* 67(12):7648-7653 (1993)), adenovirus DNA-binding protein (Zijderveid and van der Vliet, *J. Virology* 68(2):1158-1164 (1994)), herpes simplex viral protein ICP8 (Boehmer and Lehman, *J. Virology* 67(2):711-715 (1993); Skaliter and Lehman, *Proc. Natl. Acad. Sci. USA* 91(22):10665-10669 (1994)), single-stranded DNA binding proteins (SSB; Rigler and Romano, *J. Biol. Chem.* 270:8910-8919 (1995)), and calf thymus helicase (Siegel *et al.*, *J. Biol. Chem.* 267:13629-13635 (1992)).

The ability of a polymerase to carry out rolling circle replication can be determined by using the polymerase in a rolling circle replication assay

5 such as those described in Fire and Xu, *Proc. Natl. Acad. Sci. USA* 92:4641-4645 (1995).

10 It is possible to enhance the specificity of the DNA amplification reactions used in the disclosed method by using a DNA polymerase that is inactive at low temperature, and active only at high temperature. An example of such an enzyme, AmpliTaq Gold, has been described by Moretti *et al.*, *Biotechniques* 25:716-722 (1998). AmpliTaq Gold is inactive until heated during the PCR before thermal cycling. A similar enzyme could be used in the disclosed method. Temperature activation of DNA polymerase 15 can also be achieved using antibodies specific for the polymerase. For example, antibodies specific for Bst large fragment DNA polymerase could be obtained by immunization of mice. Among such antibodies, one could be chosen on the basis of its ability to bind to and inhibit the enzyme at room temperature. The antibody could also be chosen, using known screening 20 procedures, such that upon heating, the inhibition of the DNA polymerase would cease. Combining the antibody with Bst large fragment DNA polymerase would generate an enzyme mixture that is activated upon heating.

#### 30 K. Kits

20 Any combination of the materials useful in the disclosed method can be packaged together as a kit for performing the disclosed method. In particular, linear vectors, rolling circle replication primers, affinity 35 substrates, and strand displacement primers are useful components of such kits. Enzymes necessary for the disclosed method are also preferred components of such kits.

#### 40 L. Tandem Sequence DNA

45 The first strand of the circular vector, when replicated, gives rise to a long DNA molecule containing multiple repeats of sequences complementary to the circular vector. This long DNA molecule is referred to herein as tandem sequences DNA (TS-DNA). TS-DNA contains sequences 30 complementary to the inserted nucleic acid molecule and the primer complement portion. If the tandem sequence DNA is itself replicated by strand displacement amplification, the resulting long DNA molecules 50



5 containing multiple repeats of sequences matching the circular vector are referred to as secondary tandem sequence DNA. If the secondary tandem sequence DNA is in turn replicated by strand displacement amplification, the resulting long DNA molecules containing multiple repeats of sequences  
10 5 complementary to the circular vector are referred to as tertiary tandem sequence DNA.

#### M. Collected Samples (Library Replica)

15 The usefulness of the disclosed method is increased by producing libraries of clones and saving samples of the clones for later use. Such  
10 samples are referred to as collected samples. Collecting samples is analogous to replica plating in cell-based cloning. Samples of amplified nucleic acid can be collected, for example, by transfer with an array of pins (most useful  
20 when the nucleic acid is amplified in an array pattern), by transfer into an array, by direct transfer from a spread of amplified nucleic acid on a surface  
15 to another surface (this is analogous to colony transfer), and by blotting the amplified nucleic acid onto a membrane (most useful when the nucleic acid is amplified in agarose). Once the samples are collected, they can be further amplified to allow analysis or use of the clones, or to allow another round of  
25 replica collection.

#### II. Method

35 The disclosed method involves inserting nucleic acid molecules of interest into a linear vector to form a circular vector with one continuous strand and one discontinuous strand. The discontinuous strand may include  
25 an affinity tag which, by interaction with an affinity substrate, can facilitate separation of the continuous strand from the discontinuous strand. The continuous strand of the circular vector is amplified by rolling circle replication to form tandem sequence DNA. Rolling circle replication is primed by a rolling circle replication primer complementary to a sequence in  
40 the continuous strand. The tandem sequence DNA itself may be amplified by strand displacement replication, to form secondary tandem sequence DNA, using strand displacement primers (complementary to a sequence in the tandem sequence DNA). The secondary tandem sequence DNA may  
45 30

5 also be amplified by strand displacement replication, to form tertiary tandem  
sequence DNA, using strand displacement primers or the rolling circle  
replication primers (complementary to a sequence in the secondary tandem  
sequence DNA). The amplified DNA can be sequenced, probed, subjected  
10 5 to restriction analysis, subcloned, transcribed, subjected to hybridization or  
denaturation analysis, further amplified, or stored.

Multiple amplification reactions can be carried out in parallel,  
preferably in arrays or as spreads of diluted vectors on surfaces or embedded  
15 in agarose. The resulting "colonies" of amplified DNA represent molecular  
clones of the progenitor circular vectors with an inserted nucleic acid  
10 molecule. Collectively, such colonies form a library of cloned nucleic acid  
molecules that can be replica plated or arrayed, stored, and screened. These  
20 procedures are described in detail below.

When using the disclosed method to produce a library of cDNA  
15 molecules, or to analyze mRNA in a sample via cDNA, the cDNA  
25 preparations used for cloning in the disclosed vectors can be prepared using  
methods that reduce the over-representation of cDNA that corresponds to  
highly abundant messenger RNA. Libraries made using such methods are  
30 called normalized libraries (Bonaldo *et al.*, *Genome Res* 6:791-806 (1996)).  
20 The use of normalized libraries reduces the number of clones that must be  
screened to find a sequence of interest.

#### A. Ligation

35 Ligation of nucleic acid molecules into linear vectors can be  
accomplished using any suitable conditions. Techniques for insertion of  
25 nucleic acid molecules into vectors in general are well established and can be  
used with the disclosed linear vectors. Suitable ligases for the ligation  
40 operation are described above. Ligation reactions can involve a single type  
of linear vector and a single type of nucleic acid molecule to be inserted, a  
single type of linear vector and multiple different types of nucleic acid  
45 molecules to be inserted, multiple types of linear vector and a single type of  
nucleic acid molecule to be inserted, or multiple types of linear vectors and  
multiple types of nucleic acid molecules to be inserted. For general cloning  
50 and production of nucleic acid libraries it is preferred that a single type of

linear vector and multiple different types of nucleic acid molecules to be inserted be used. For subcloning of specific nucleic acid fragments it is preferred that a single type of linear vector and a single type of nucleic acid molecule to be inserted. Ligation conditions are generally known. Most ligases require  $Mg^{++}$ . There are two main types of ligases, those that are ATP-dependent and those that are NAD-dependent. ATP or NAD, depending on the type of ligase, should be present during ligation.

Ligation of compatible ends of nucleic acid molecules and vectors can be facilitated through the use of blunt ends or sticky ends as is known in the field of molecular cloning. Both blunt ends and sticky ends can be produced by digestion of the nucleic acid molecules and the linear vectors with appropriate restriction enzymes, by ligation of appropriate linkers to the ends of the nucleic acid molecules and the linear vectors, or both. In the case of linear vectors, appropriate ends can be formed directly by the structure of the linear vector without the need for restriction enzyme digestion of linker ligation. In the case of the nucleic acid molecules to be inserted, appropriate ends can be appended to the ends during preparation of the nucleic acid molecule. For example, appropriate ends can be incorporated into cDNA by using primer having appropriate sequences during cDNA synthesis or by adding a nucleotide tail to the cDNA.

#### B. Amplification

The circular vectors formed by ligation of linear vectors and nucleic acid molecules of interest serve as substrates for a rolling circle replication. This reaction requires the addition of two reagents: (a) a rolling circle replication primer, which is complementary to the primer complement portion of the first strand of the circular vector, and (b) a rolling circle DNA polymerase. The DNA polymerase catalyzes primer extension and strand displacement in a processive rolling circle polymerization reaction that proceeds as long as desired, generating a molecule of up to 100,000 nucleotides or larger that contains up to approximately 25 tandem copies of a sequence complementary to a 4000 bp circular vector. This tandem sequence DNA (TS-DNA) consists of alternating vector sequence and insert

5 sequence. As an alternative, the second strand of the circular vector can serve as the rolling circle replication primer.

During rolling circle replication one may additionally include radioactive, or modified nucleotides such as bromodeoxyuridine triphosphate, in order to label the DNA generated in the reaction. Alternatively, one may include suitable precursors that provide a binding moiety such as biotinylated nucleotides (Langer *et al.*, *Proc. Natl. Acad. Sci. USA* 78:6633 (1981)).

Strand displacement replication is a way to amplify TS-DNA. Strand displacement replication is accomplished by hybridizing strand displacement primers to TS-DNA and allowing a DNA polymerase to synthesize DNA from these primed sites. The product of strand displacement replication is referred to as secondary tandem sequence DNA or TS-DNA-2. Strand displacement replication can be accomplished by performing rolling circle replication to produce TS-DNA, and then mixing strand displacement primer with the TS-DNA and incubating to replicate the tandem sequence DNA. The strand displacement primer is complementary to a part of the circular vector used to generate TS-DNA as described earlier. It is preferred that the strand displacement primer is not complementary to the rolling circle replication primer, or to a tertiary strand displacement primer, if used.

Strand displacement replication can also be carried out simultaneously with rolling circle replication. This is accomplished by mixing strand displacement primer with the circular vector and rolling circle replication primer prior to incubating the mixture for rolling circle replication. For simultaneous rolling circle replication and strand displacement replication, it is preferred that the rolling circle DNA polymerase be used for both replications. This allows optimum conditions to be used and results in displacement of other strands being synthesized downstream. Generally, strand displacement replication can be performed by, simultaneous with or following rolling circle replication, mixing a strand displacement primer with the TS-DNA and incubating to replicate the tandem sequence DNA to result in the formation of secondary tandem sequence DNA.

5 To optimize the efficiency of strand displacement replication, it is preferred that a sufficient concentration of strand displacement primer be used to obtain sufficiently rapid priming of the growing TS-DNA strand to out-compete any remaining unligated linear vectors that might be present for  
10 5 binding to TS-DNA. In general, this is accomplished when the strand displacement primer is in very large excess compared to the concentration of single-stranded sites for hybridization of the strand displacement primer on TS-DNA. Optimization of the concentration of strand displacement primer can be aided by analysis of hybridization kinetics using methods such as  
15 those described by Young and Anderson, "Quantitative analysis of solution hybridization" in *Nucleic Acid Hybridization: A Practical Approach* (IRL Press, 1985) pages 47-71. Alternatively, the efficiency of strand displacement replication can be improved by the removal of unligated linear vectors prior to amplification of the TS-DNA. In strand displacement  
20 replication, it is preferred that the concentration of strand displacement primer generally be from 500 nM to 5000 nM, and most preferably from 700 nM to 1000 nM.

30 As a strand displacement primer is elongated, the DNA polymerase will run into the 5' end of the next hybridized strand displacement molecule and will displace its 5' end. In this fashion a tandem queue of elongating DNA polymerases is formed on the TS-DNA template. As long as the rolling circle reaction continues, new strand displacement primers and new  
35 DNA polymerases are added to TS-DNA at the growing end of the rolling circle.

25 When strand displacement replication is carried out in the presence of a tertiary strand displacement primer, an exponential amplification of TS-DNA sequences takes place. This special and preferred mode of strand displacement replication is referred to as strand displacement cascade amplification (SDCA). In SDCA, a strand displacement primer primes  
40 replication of TS-DNA to form TS-DNA-2, as described above. The tertiary strand displacement primer can then hybridize to, and prime replication of, TS-DNA-2 to form TS-DNA-3 (tertiary tandem sequence DNA). Strand displacement of TS-DNA-3 by the adjacent, growing TS-DNA-3 strands  
50

5 makes TS-DNA-3 available for hybridization with secondary strand displacement primer. This results in another round of replication resulting in TS-DNA-4 (which is equivalent to TS-DNA-2). TS-DNA-4, in turn, becomes a template for DNA replication primed by tertiary strand  
10 displacement primer. The cascade continues this manner until the reaction stops or reagents become limiting. This reaction amplifies DNA at an almost exponential rate, although kinetics are not truly exponential because there are stochastically distributed priming failures, as well as steric hindrance events related to the large size of the DNA network produced during the reaction.

15 In a preferred mode of SDCA, the rolling circle replication primer serves as the tertiary strand displacement primer, thus eliminating the need for a separate primer. For this mode, the rolling circle replication primer should be used at a concentration sufficiently high to obtain rapid priming on the growing TS-DNA-2 strands. To optimize the efficiency of SDCA, it is  
20 preferred that a sufficient concentration of secondary strand displacement primer and tertiary strand displacement primer be used to obtain sufficiently rapid priming of the growing TS-DNA strand to out-compete TS-DNA for binding to its complementary TS-DNA, and, in the case of secondary strand displacement primer, to out-compete any remaining unligated linear vector  
25 that might be present for binding to TS-DNA. In general, this is accomplished when the secondary strand displacement primer and tertiary strand displacement primer are both in very large excess compared to the concentration of single-stranded sites for hybridization of the strand displacement primers on TS-DNA. For example, it is preferred that the  
30 secondary strand displacement primer is in excess compared to the concentration of single-stranded secondary strand displacement primer complement sites on TS-DNA, TS-DNA-3, TS-DNA-5, and so on. In the case of tertiary strand displacement primer, it is preferred that the tertiary strand displacement primer is in excess compared to the concentration of  
35 single-stranded tertiary strand displacement primer complement sites on TS-DNA-2, TS-DNA-4, TS-DNA-6, and so on. Such an excess generally results in a primer hybridizing to its complement in TS-DNA before amplified complementary TS-DNA can hybridize. Optimization of primer

5 concentrations can be aided by analysis of hybridization kinetics (Young and Anderson). In a strand displacement cascade amplification, it is preferred that the concentration of both secondary and tertiary strand displacement primers generally be from 500 nM to 5000 nM, and most preferably from 10 5 700 nM to 1000 nM.

As in the case of secondary strand displacement primers, if the concentration of DNA polymerase is sufficiently high, the polymerase will initiate DNA synthesis at each available 3' terminus on the hybridized 15 tertiary strand displacement primers, and these elongating TS-DNA-3 10 molecules will block any hybridization by TS-DNA-2. As a tertiary strand displacement primer is elongated to form TS-DNA-3, the DNA polymerase will run into the 5' end of the next hybridized tertiary strand displacement primer molecule and will displace its 5' end. In this fashion a tandem queue of elongating DNA polymerases is formed on the TS-DNA-2 template. As 20 long as the reaction continues, new rolling circle replication primers and new DNA polymerases are added to TS-DNA-2 at the growing ends of TS-DNA-2. This hybridization/replication/strand displacement cycle is repeated with hybridization of secondary strand displacement primers on the growing TS-DNA-3. 25

30 Generally, strand displacement cascade amplification can be performed by, simultaneous with, or following, rolling circle replication, mixing a secondary strand displacement primer and a tertiary strand displacement primer with the TS-DNA and incubating to replicate the 35 tandem sequence DNA -- where replication of the tandem sequence DNA results in the formation of secondary tandem sequence DNA and where 25 replication of the secondary tandem sequence DNA results in formation of tertiary tandem sequence DNA (TS-DNA-3). 40

Strand displacement replication can also be carried out sequentially. Following a first round of strand displacement replication, a tertiary strand 45 displacement primer can be mixed with the TS-DNA and TS-DNA-2 and incubated to replicate the secondary tandem sequence DNA, where replication of the secondary tandem sequence DNA results in formation of tertiary tandem sequence DNA (TS-DNA-3). This round of strand 50

displacement replication can be referred to as tertiary strand displacement replication. However, all rounds of strand displacement replication following rolling circle replication can also be referred to collectively as strand displacement replication.

A modified form of strand displacement replication results in amplification of TS-DNA and is referred to as opposite strand amplification (OSA). OSA is the same as strand displacement replication except that a special form of rolling circle replication primer is used that prevents it from hybridizing to TS-DNA-2. This can be accomplished in a number of ways. For example, the rolling circle replication primer can have an affinity tag coupled to its non-complementary portion allowing the rolling circle replication primer to be removed prior to strand displacement replication. Alternatively, remaining rolling circle replication primer can be crippled following initiation of rolling circle replication. One preferred form of rolling circle replication primer for use in OSA is designed to form a hairpin that contains a stem of perfectly base-paired nucleotides. The stem can contain 5 to 12 base pairs, most preferably 6 to 9 base pairs. Such a hairpin-forming rolling circle replication primer is a poor primer at lower temperature (less than 40°C) because the hairpin structure prevents it from hybridizing to complementary sequences. The stem should involve a sufficient number of nucleotides in the complementary portion of the rolling circle replication primer to interfere with hybridization of the primer to the circular vector. Generally, it is preferred that a stem involve 5 to 24 nucleotides, and most preferably 6 to 18 nucleotides, of the complementary portion of a rolling circle replication primer. A rolling circle replication primer where half of the stem involves nucleotides in the complementary portion of the rolling circle replication primer and the other half of the stem involves nucleotides in the non-complementary portion of the rolling circle replication primer is most preferred. Such an arrangement eliminates the need for self-complementary regions in the circular vector when using a hairpin-forming rolling circle replication primer.

If an excess of tertiary tandem sequence DNA is desired, the secondary strand displacement primer can be crippled in the same manner as



5 is described above for the rolling circle replication primer (the rolling circle replication primer and tertiary strand displacement primer should not be crippled in this case). The reaction at the higher, permissive temperature should be carried out long enough to produce a reasonable amount of  
10 5 secondary tandem sequence DNA to serve as a template for tertiary sequence DNA. When the temperature is shifted, the secondary strand displacement primer can no longer prime synthesis and the synthesis of tertiary tandem sequence DNA soon outstrips the amount of secondary tandem sequence  
15 DNA. Of course tandem sequence DNA will continue to be produced by  
10 rolling circle replication throughout the reaction (since the rolling circle replication primer is not crippled).

20 When starting the rolling circle replication reaction, secondary strand displacement primer and rolling circle replication primer are added to the reaction mixture, and the solution is incubated briefly at a temperature  
15 sufficient to disrupt the hairpin structure of the rolling circle replication primer but to still allow hybridization to the primer complement portion of the circular vector (typically greater than 50°C). This incubation permits the rolling circle replication primer to hybridize to the primer complement  
25 portion of the circular vector. The solution is then brought to the proper  
30 temperature for rolling circle replication, and the rolling circle DNA polymerase is added. As the rolling circle reaction proceeds, TS-DNA is generated, and as the TS-DNA grows in length, the secondary strand displacement primer rapidly initiates DNA synthesis with multiple strand displacement reactions on TS-DNA. These reactions generate TS-DNA-2,  
35 which is complementary to the TS-DNA. While TS-DNA-2 contains  
25 sequences complementary to the rolling circle replication primer, the primer is not able to hybridize nor prime efficiently at the reaction temperature due to its hairpin structure at this temperature. Thus, there is no further priming by the rolling circle replication primer and the only products generated are  
40 TS-DNA and TS-DNA-2. The reaction comes to a halt as rolling circle amplification stops and TS-DNA becomes completely double-stranded. In the course of the reaction, an excess of single-stranded TS-DNA-2 is  
45 generated.  
50

Another form of rolling circle replication primer useful in OSA is a chimera of DNA and RNA. In this embodiment, the rolling circle primer has deoxyribonucleotides at its 3' end and ribonucleotides in the remainder of the primer. It is preferred that the rolling circle replication primer have five or six deoxyribonucleotides at its 3' end. By making part of the rolling circle replication primer with ribonucleotide, the primer can be selectively degraded by RNase H when it is hybridized to DNA. Such hybrids form during OSA as TS-DNA-2 is synthesized. The deoxyribonucleotides at the 3' end allow the rolling circle DNA polymerase to initiate rolling circle replication. RNase H can then be added to the OSA reaction to prevent priming of TS-DNA-2 replication.

Unligated linear vectors may be removed prior to rolling circle replication to eliminate competition between unligated linear vectors and the secondary strand displacement primer for hybridization to TS-DNA.

Alternatively, the concentration of the secondary strand displacement primer can be made sufficiently high so that it out-competes unligated linear vector for hybridization to TS-DNA. This allows strand displacement replication to be performed without removal of unligated linear vectors.

#### C. Separation

Once the linear vector and nucleic acid molecule are circularized to form a circular vector with one continuous strand and one discontinuous strand, it is preferred that the continuous strand of the circular vector (a single-stranded, closed circular nucleic acid molecule susceptible to rolling circle replication) is separated from the discontinuous strand of the circular vector. Separation allows rolling circle replication to proceed more efficiently.

It is preferred that the two strands of the circular vector are separated by immobilizing the discontinuous (second) strand of the circular vector and then denaturing and washing away the continuous (first) strand of the circular vector. This can be accomplished, for example, by including an affinity tag in the second strand of the circular vector which can then be bound to an immobilized affinity target, thus immobilizing the second strand

5 of the circular vector. For this purpose, use of biotin as an affinity tag and streptavidin as an affinity target is preferred.

Complementary oligonucleotides can also be used as binding pairs for separating the first and second strands of the circular vector. An  
10 5 oligonucleotide affinity tag that is a part of or coupled to the second strand of the circular vector is hybridized to an immobilized complementary oligonucleotide. The oligonucleotide affinity tag is preferably an unhybridized tail in an overlap in the second strand of the circular vector (see  
15 Figure 3). It is preferred that the oligonucleotide affinity tag be ligated or otherwise coupled to a solid-state substrate or support to keep the second strand immobilized during denaturation. This can be accomplished, for  
20 example, by using a circular vector with a staggered tail in the second strand and an immobilized oligonucleotide that can hybridize to the longer strand of the tail such that the end of the immobilized oligonucleotide can be ligated to  
15 the shorter strand of the staggered tail. An example of such an arrangement is shown in Figure 3.

The first and second strands of the circular vector can be denatured using any suitable means. Preferred conditions for denaturation include the  
30 use of heat, alkaline conditions, chaotropic conditions, and combinations. These and other means of nucleic acid denaturation are known and can be  
20 used in the disclosed method. Washing and collection of the first strand is performed during or after denaturation.

As an example, the first and second strands of circular can be separated using a two-step procedure. First, the circular vector, which  
35 contains a biotin residue on the second strand, is bound to beads containing streptavidin, in order to bind the vector via the biotin. The beads are then washed with formamide at mildly alkaline pH. Under appropriate  
40 conditions, the circular vector, which contains an unligated nick site by design, separates into two DNA molecules. Thus, alkaline denaturation releases free single-stranded circles from the beads. The single-stranded  
45 30 circular molecules (that is, the first strands of the circular vector) are then further purified by gel filtration or ion exchange (Mono-Q 5/5) chromatography in the presence of an alkaline buffer (15 mM NaOH). This  
50

purification step will remove small circles, and small linear vector molecules that contaminate the circular vectors with inserts.

#### D. Removing Linear Nucleic Acids

Unligated linear nucleic acids, including unligated linear vector, can be removed prior to rolling circle replication. In addition to methods described elsewhere herein, the gene 6 exonuclease of phage T7 provides a useful tool for the elimination of linear nucleic acids that might bind to the TS-DNA. This exonuclease digests DNA starting from the 5' end of a double-stranded structure. It has been used successfully for the generation of single-stranded DNA after PCR amplification (Holloway *et al.*, *Nucleic Acids Res.* 21:3905-3906 (1993); Nikiforov *et al.*, *PCR Methods and Applications* 3:285-291(1994)). This enzyme can be added after ligation, together with the rolling circle DNA polymerase. To protect TS-DNA from degradation, the rolling circle replication primer can contain 3 or 4 phosphorothioate linkages at the 5' end, to make this molecule resistant to the exonuclease (Nikiforov *et al.* (1994)). The exonuclease will degrade unprotected linear molecules as they become associated with the rolling circle DNA product.

#### E. Dilution and Division

The disclosed method is particularly useful for creation of a library of cloned nucleic acid molecules. For this purpose it is useful to dilute and divide ligated vectors containing inserts to separate individual circular vectors and allow production of clonal "colonies" of nucleic acid amplified from a single circular vector. It is preferred that a solution containing circular vectors is diluted sufficiently such that amplification reactions contain, on average, a single circular vector. This can be accomplished, for example, by making a range of dilutions, dividing the diluted vector solutions among reactions, and performing amplification. The dilution is considered optimal when about 33% of the reactions produce amplified nucleic acid. This follows from well known distribution statistics.

The division of the diluted circular vectors can be accomplished in several ways. For example, the diluted solution can be spotted as an array on a surface. The diluted solution can also be spread on a surface with the

5 circular vectors becoming separated. The diluted solution can also be mixed  
with agarose and spread on a surface. A preferred way to divide the diluted  
10 circular vectors is to use a microarray of very small liquid droplets on a glass  
surface. The micro-droplet arrays contain the diluted circular vectors, and  
5 enable the generation of DNA clones in very small compartments, without  
the need for physical barriers such as tubes or wells.

One useful way to combine division of the ligation reaction with  
15 amplification is to spread the ligation reaction (diluted or not as appropriate)  
on a surface and then to spot amplification reaction components (that is,  
10 buffers, reagents, polymerase) on the surface in an array. Techniques for  
spotting are described, for example, in U.S. Patent No. 5,807,522 to Brown  
20 et al. The method here differs, however, in that it is the reaction  
components, rather than individual samples, that are spotted. All of the  
spotted material is identical. The amplification reagents will then cause  
25 amplification of whatever nucleic acid is present at the location of each spot  
of reagents. The nucleic acid on the surface comes from the spread of the  
ligation reaction.

As an example of spreading, the ligated DNA can be diluted serially  
30 to obtain concentrations in the range of several million molecules per  
milliliter. Approximately 22  $\mu$ l of this DNA solution (containing  
20 approximately 30,000 to 120,000 DNA molecules) is placed on a cover slip,  
and covered with a polylysine-coated microscope slide. The DNA is allowed  
35 to bind the polylysine-covered surface for 30 minutes at 37°C. The slide  
then dipped in 0.01% Tween-20, and dried at room temperature. Using an  
arraying instrument, an array is constructed consisting of 6000 individual  
40 micro-droplets of a solution containing the four dideoxynucleoside  
triphosphates, a suitable buffer, and enzymes for amplification. The  
diameter of the droplets can be approximately 0.150 millimeters. Droplets  
45 preferably are dispensed on the surface of the slide in a controlled humidity  
atmosphere, in order to maintain a constant droplet volume during  
30 amplification. Alternatively, the diluted circular vectors may be placed on  
the glass surface using the arrayer instrument to dispense small volumes that  
50 on the average contain a single ligated DNA molecule. It can be calculated

5 that when 33% of the droplets grow molecular colonies, and the rest do not grow anything, most colonies are likely to be of clonal origin. Adjusting the initial inoculum density, it should be possible to obtain up to 1500 clonal colonies per 6000-droplet array.

10 5 As an example of agarose spreading, dilutions of the vectors can be mixed with a buffer containing melted agarose at 60°C and overlaying the solution on a petri dish to form a thin agarose layer (0.2 to 2% agarose), such that the concentration of the vectors is in the range of 500 to 5,000 per plate. The embedded vectors can then be amplified using the disclosed method. At 15 appropriate dilutions, DNA molecular colonies clonally derived from single vectors will form in the thin film of agarose. The initial density of seed DNA molecules should be such that the DNA molecular colonies do not overlap. One useful technique of agarose spreading is describe in U.S. Patent No. 5,616,478 to Chetverin et al.

#### 25 15 F. Sample Collection (Replica Plating)

The usefulness of the disclosed method is increased by producing libraries of clones and saving samples of the clones for later use. Such samples are referred to as collected samples. Collecting samples is 30 analogous to replica plating in cell-based cloning. Samples of amplified nucleic acid can be collected, for example, by transfer with an array of pins (most useful when the nucleic acid is amplified in an array pattern), by transfer into an array, by direct transfer from a spread of amplified nucleic acid on a surface to another surface (this is analogous to colony transfer), and by blotting the amplified nucleic acid unto a membrane (most useful when 35 the nucleic acid is amplified in agarose). Once the samples are collected, they can be further amplified to allow analysis or use of the clones, or to allow another round of replica collection.

40 25 Where droplet arrays are used, the molecular colonies (that is, the droplets following amplification) can be replicated by contacting the array with a multi-pin replicator that will bind only a fraction of the volume of the micro-droplet. Colony replicas may be stored by blotting the replicator on a membrane such as nitrocellulose of NA-45 (S&S). A preferred way to store replicas is to contact the replicator with a polylysine-coated glass slide, 50

5 which will permit hybridization or primer extension sequencing with  
fluorescent probes. Replicas of reaction droplets on a surface can also be  
made by contacting a second surface with the droplets. In general, it is  
10 preferred that the second surface contact only the droplets and not the first  
5 surface. Replicas of spreads of nucleic acids on a surface likewise can be  
made by contacting a second surface with the spread.

Replicas of amplified nucleic acid bound covalently to glass can be  
made using any suitable coupling procedure. For example, in order to  
15 facilitate a subsequent step of covalent binding to a glass surface, each of the  
two strand displacement replication primers used for the strand displacement  
10 cascade amplification of circular vectors may be synthesized with a primary  
amino group at the 5' end. At the end of the amplification reaction, the glass  
slide will contain thousands of liquid droplets harboring DNA clones, and all  
20 the DNA molecules will contain 5'-terminal reactive amino groups. At this  
point the glass slide can be contacted with another glass slide, leaving an air  
25 gap of less than 1 mm (defined by the thickness of a plastic spacer), in such a  
manner that the glass slide on top will contact all of the liquid droplets  
without excessive compression. The lower face of this slide (the upper slide)  
can be derivatized using the methods described by Guo *et al.*, *Nucleic Acids*  
30 *Research* 22:5456-5465 (1994), Guo *et al.*, *Nature Biotechnology*  
15:331-335 (1997), Guo *et al.*, *Nucleic Acids Res* 22:5456-5465 (1994), or  
Beier and Hoheisel, *Nucleic Acids Res* 27:1970-1977 (1999), to make the  
35 glass surface chemically reactive. The two-slide sandwich is incubated for 1  
to 2 hours at 37°C (or as appropriate for the derivative chemistry involved)  
25 in order to obtain covalent coupling of the amplified DNA contained in each  
droplet to the lower face of the upper slide.

Where agarose has been used to form molecular colonies, analysis of  
the colonies can be facilitated by blotting the amplified nucleic acid unto a  
membrane or other blotting surface. Many such blotting techniques are  
45 known and can be used with the disclosed method. For example, the agarose  
film can be placed in a vacuum-blotting device that contacts both the bottom  
and the top of the agarose film. The nucleic acid on the agarose film can  
50 then be vacuum-blotted to two membranes simultaneously, one placed on top

5 of the agarose and the other below the agarose, to generate two replicas of the molecular colonies on the surface of the membrane.

#### G. Detecting Amplified Nucleic Acid Molecules

10 The amplified nucleic acid can be used for any purpose for which nucleic acids can be used. For example, the nucleic acid can be sequenced, probed, subjected to restriction analysis, subcloned, transcribed, subjected to hybridization or denaturation analysis, further amplified, or stored. Diagnostic methods, such as sequencing and probing for specific sequences, 15 are preferred. For these purposes, the amplified nucleic acid can be analyzed using standard molecular biology procedures, such restriction enzyme digestion, cloning in a plasmid vector, PCR amplification, which are well known. 20

Libraries of cloned nucleic acids formed by the disclosed method can be screened using any of the methods used for screening conventional 15 libraries. For example, cDNA libraries made using the disclosed method can be analyzed using conventional screens. Libraries can also be used for *in situ* transcription to generate RNA colonies, which can then be analyzed (*in situ* or in replicas) by appropriate screens, such as aptamer screens or ribozyme activity screens. Libraries can also be screened by *in situ* 20 translation on array replicas (see, for example, Saris *et al.*, *Nucleic Acids Res.* 10:4831-4843 (1982)). Libraries can also be screened by *in situ* coupled transcription-translation systems, and subsequent catalytic activity assays for the analysis of mutagenized enzymes. 35

The disclosed method can also be used for serial analysis of gene 25 expression (SAGE), making it more efficient by streamlining the cloning and sequencing into a single process stream. This method involves amplification of cDNA inserted into linear vectors as described herein prior to the SAGE analysis. This means of amplification is useful since PCR amplification of the cDNA prior to cloning, which can skew the abundance of cDNA 40 sequences due to differential amplification, is avoided. The disclosed method insures that sequence tag frequencies in the clone population (which are measured in SAGE) reflect the original frequencies of the cDNAs. 45



5 The method of Welford *et al.*, *Nucleic Acids Res.* 26(12):3059-3065  
(1998), in which thousands of colonies produced using laborious traditional  
procedures were analyzed in an array, can be modified to make use of the  
disclosed method and thereby become more streamlined and efficient. The  
10 method could even be automated. Detection of differences between nucleic  
acid samples or probe sets can be accomplished by adapting the technique  
described by George *et al.*, *Nucleic Acids Research* 27:1517-1523 (1999), to  
the disclosed method. George *et al.* describes combination of suppression  
15 subtractive hybridization (SSH) and cDNA microarrays for rapid  
identification of differentially expressed genes. In this method, a set of  
cDNA clones, including inserts amplified by PCR, is arrayed using robotic  
printing. The cDNA arrays can then be hybridized with fluorescent labeled  
20 probes prepared from RNA obtained from a cell line or tissue of interest.

#### H. Sequencing Amplified Nucleic Acid Molecules

15 The amplified nucleic acid can be sequenced using any suitable  
procedure. Many such procedures are known. One preferred form of  
sequencing for use with amplified sequences produced with the disclosed  
method is nanosequencing or single-nucleotide extension sequencing.  
20 Nanosequencing methods are described below and by Jalanko *et al.*, *Clinical  
Chemistry* 38:39-43 (1992); Nikiforov *et al.*, *Nucleic Acids Research*  
22:4167-4175 (1994); and Kobayashi *et al.*, *Molecular and Cellular Probes*  
9:175-182 (1995).

35 Two forms of primer extension sequencing that can be used with the  
disclosed method are described in PCT Application WO 97/20948. One is  
25 single nucleotide primer extension sequencing involving interrogation of a  
single nucleotide in an amplified target sequence by incorporation of a  
specific and identifiable nucleotide based on the identity of the interrogated  
30 nucleotide. The other is degenerate probe primer extension sequencing  
involving sequential addition of degenerate probes to an interrogation primer  
hybridized to amplified target sequences.

Nanosequencing operations can be performed in batch. For example,  
if the slide contains 3000 dots, all 3000 dots are sequenced in a single batch  
operation. This can be accomplished by washing the slide with 1% ammonia

after imaging of the first primer extension reaction. This alkaline solution denatures the labeled primer, but the cloned DNA remains on the slide because it is bound covalently. The subsequent primer extension reactions are performed, imaged, and washed with ammonia at each step until all five primers have been extended and the fluorescence incorporated by the primer has been imaged at each step.

The next step consists of determining a very short stretch of nucleotide sequence in the amplified DNA in each replica on the nitrocellulose. This entails sequencing just nine bases in a clone (which are referred to as the sequence tag of the clone). In this example, this is accomplished by two separate sets of sequencing reactions taking place in each replica-membrane. One set of sequencing reactions will determine the first five bases in the upper strand of the clone. The other set of sequencing reactions will determine the first five bases in the lower strand of the clone (always reading 5' to 3') as shown by the underlined X's below.

```

                >>>>>
5' - NNNNNNNNNNNNNNNXXXXXXXXXXNNNNNNNNNNNNNNNNNNNN - 3'
3' - NNNNNNNNNNNNNNNXXXXXXXXXXNNNNNNNNNNNNNNNNNNNN - 5'
                <<<<<<

```

Each stretch of five bases is interrogated by using a mixture of specific primers for each base to be sequenced, using a single addition of a dideoxynucleotide triphosphate (ddNTP). The 3' end of the first primer (Primer 1) is positioned just before the first base to be sequenced. The sequence of the primer is defined by complementarity to vector sequences flanking the insert (or non-variable sequences flanking the region to be sequenced). The 3' end of the second primer (Primer 2) is positioned just before the second base to be sequenced. The sequence of the Primer 2 is defined by complementarity to the flanking sequences, but the last base at the 3' end is degenerate. A example design for Primer 1, Primer 2, and subsequent primers is shown below. The letter N indicates interrogation bases in a clone. The letter D indicates a degenerate base position in the primer. The question mark (?) indicates the nucleotide to be added to the primer.

Cloned sequence (SEQ ID NO:1):

TAAGTCTAGTTGACAGGATGCATGNNNNNNNNNccagacagttgttgactgatggtg  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

Primer 1 (complexity = 1) (SEQ ID NOs:2 and 1)

TCTAGTTGACAGGATGCATG?  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

Primer 2 (complexity = 4) (SEQ ID NOs:3 and 1)

CTAGTTGACAGGATGCATGD?  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

Primer 3 (complexity = 16) (SEQ ID NOs:4 and 1)

TAGTTGACAGGATGCATGDD?  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

Primer 4 (complexity = 64) (SEQ ID NOs:5 and 1)

AGTTGACAGGATGCATGDDD?  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

Primer 5 (complexity = 256) (SEQ ID NOs:6 and 1)

GTTGACAGGATGCATGDDDD?  
ATTGAGATCAACTGTCCTACGTACNNNNNNNNNagctctgtcaacaactgactaccgac

While primer 1 is not degenerate, primer 2 contains one degenerate position, primer 3 contains two degenerate positions, primer 4 contains three degenerate positions, and primer 5 contains four degenerate positions.

Although primers 4 and 5 may prime at incorrect positions, the low complexity of the amplified DNA in a DNA colony produced by the disclosed method tends to ensure correct priming reads, on the average.

Primer extension is carried out for 5 minutes at 38°C in a primer extension solution containing Primer 1 as the only primer. The primer extension mixture preferably contains a thermostable DNA polymerase such as Taq polymerase, and a mixture of four fluorescent dideoxy-oligodeoxyribonucleotides, each labeled with a different dye, as in standard fluorescent sequencing (Perkin Elmer-Applied Biosystems, Inc.). Because only dideoxynucleotides are present in each colony replica, and because the colony contains millions of copies of the nucleic acid sequence of interest, the added fluorescent label will be easily detectable for each reaction. After

5

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40

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5 The short five-base sequences on each end, together with the sequences of flanking restriction enzyme sites, are sufficient to serve the function of unique tagging of each cDNA clone using the procedures described above.

10 Replica-binding of amplified nucleic acid molecules to glass slides, as described elsewhere herein, enables sequencing using a single slide. This is accomplished by washing the slide with 1% ammonia after imaging of the first primer extension reaction. This alkaline solution denatures the labeled primer, but the cloned nucleic acid remains on the slide because it is bound covalently. The subsequent primer extension reactions are performed, 15 imaged, and washed with ammonia at each step until all five primers have been extended and the fluorescence incorporated by the primer has been imaged at each step.

20 An alternative method to read the output of nanosequencing reactions is to use mass spectroscopy instead of fluorescence. The use of mass spectroscopy for sequence identification of primers that have been extended by only one base has been described by Haff and Smirnov, *Genome Research* 7: 378-388 (1997).

25 The sequencing scheme shown above can permit the sequencing of a population of cDNA molecules derived from a single type of mRNA molecules. This can be accomplished, for example, as follows. First, a specific mRNA is amplified from any biological source using RT-PCR to obtain full-length amplification products. The amplified PCR product may have been derived from a mixture of wild-type sequence transcripts and also a small proportion (1/100, for example) of mutant transcripts that contain a single point mutation at a specific locus. Any other DNA fragment can also be used.

30 The PCR product is then nicked with DNase I to generate a random population of DNA fragments. The DNA is nick-translated with Klenow DNA polymerase to generate a population of DNA fragments in the range of 120 to 200 nucleotides. This population of subsequences generated from the population of cDNA is then cloned into linear vectors to form circular vectors and the strands of the circular vectors separated as described herein. Vectors with inserts in the size range of 120 to 200 base pairs can be isolated

(preferably before strand separation) by gel electrophoresis, or, preferably, by chromatography in Mono-Q 5/5/ (Pharmacia-LKB). The circular vectors are then amplified as described herein and the sequence of the ends of the inserts (which are thus the sequence tags) is determined as described above.

The sequence tags obtained from each clone consist of two pentamer (or even two hexamer) sequences. These sequence tags, which are known to be separated by segments of 120 to 200 bases, are catalogued and assembled into a contiguous sequence using techniques developed for hybridization sequencing. Starting with a cDNA product of a single type of mRNA, the cDNA can be entirely sequenced by assembling a catalog of sequenced clones. The sequence obtained from each clone is a pair of non-adjacent pentamers or hexamers. When a large number of molecular clones are analyzed, the method can reveal the presence of point mutations, even if they are present as 1/100th of the cDNA population.

Starting with a complex mixture of cDNAs, small DNA segments (sequence tags) present in clones that originated from individual cDNA molecules in the cDNA population can be sequenced *in situ* using a similar procedure. The method can be scaled up by increasing the density of molecular colonies, and the number of colony replicas.

#### **I. Illustrations of the Method**

The disclosed method is further illustrated by the following examples.

##### **Illustration 1: Cloning using a linker**

A DNA sample is amplified by PCR using standard procedures, except that both oligonucleotide primers are designed to contain unique restriction enzyme sites, such that after amplification the PCR product may be cleaved, generating different sticky ends on each side of the linear DNA product. One of the PCR primers additionally contains a spacer sequence. The digested PCR product is then placed in a ligation mixture containing linkers designed to circularize the amplified DNA. The linkers represent the linear vector. The linkers are designed with a chemically modified terminus in one of the oligonucleotides, such that after ligation the resulting circular DNA molecules (that is circular vectors) will contain a single nick (or

5 several nicks, if more than one linker is incorporated by ligation) in one of the strands. The modifier group may be a biotin, and it may be located either at the 5' or the 3' end of one of the linker oligonucleotides.

10 5 One of the PCR primers can also contain additional non-priming sequence designed to constitute the small spacer or backbone of the circular vector to allow amplification by rolling circle replication. The spacer sequence preferably contains a site for a rare-cutter restriction enzyme, which can be used to regenerate circles from linear DNA produced by amplification.

15 10 Optionally, the continuous strand of the circular vector can be separated from the discontinuous strand and unligated vector pieces using a two-step procedure. First, the circular vector, which contains a biotin residue, is bound to beads containing streptavidin, in order to bind the vector via the biotin present in one of the DNA strands that comprise the circular vector. The beads are then washed with formamide at mildly alkaline pH. Under appropriate conditions, the circularized DNA, which contains an unligated nick site by design, separates into two DNA molecules. Thus, mild alkaline-formamide denaturation releases free single-stranded circles from the beads. The single-stranded circular molecules are then further purified by gel filtration or ion exchange (Mono-Q 5/5) chromatography in the presence of an alkaline buffer (15 mM NaOH). This purification step will remove small linear molecules that contaminate the circular vector (which contain inserted nucleic acid molecules). The purpose of the purification procedure is useful for selecting certain DNA size classes, because this is desirable in certain applications. This separation is optional and the procedure can be performed with out strand separation or purification.

20 25 Dilutions of the DNA are then mixed with a buffer containing two primers (at approximately 1  $\mu$ Molar concentration) designed for strand displacement cascade amplification (that is, a secondary strand displacement primer and a rolling circle replication primer/tertiary strand displacement primer) and melted agarose at 60°C. The solution is overlayed on a petri dish to form a thin agarose layer (1.0% to 2% agarose), such that the concentration of circular DNA molecules is in the range of 500 to 5,000 per

5 plate. Then enzymes and dNTPs required to initiate rolling circle replication  
are then added. The agarose film is incubated for 0.5 to 3 hours at 38°C (if  
the enzyme used is exo-Klenow) or at 60°C (if the enzyme used is exo (-)  
Bst or exo (-) Bca; Walker *et al.* (1992); Walker, IBC International  
10 Conference, December, 1996). At appropriate dilutions, molecular  
"colonies" clonally derived from single circular vectors bearing DNA that  
originated in the PCR-amplified product, will form in the thin film of  
agarose. The initial density of seed DNA molecules should be such that the  
15 molecular colonies do not overlap.

20 In a preferred embodiment, one of the primers used in the  
amplification reaction is capable of forming a secondary structure. By  
lowering the temperature from 60°C to 50°C, this special primer forms a  
hairpin structure that interferes with priming while the other primer  
continues to function normally. As the amplification reaction is continued  
25 for another 45 minutes, a large proportion of the DNA product becomes  
single-stranded DNA generated by strand displacement driven by the single  
functional primer. In this way, during the latter phase of the amplification  
reaction a large proportion of the DNA contained in each colony becomes  
30 single-stranded.

35 After amplification, the agarose film is placed in a vacuum-blotting  
device with a membrane that contacts the bottom of the agarose film. Part of  
the DNA on the agarose film is vacuum-blotted onto the membrane. This  
generates a replica of the DNA colonies on the surface of the membrane.  
Blotting is carried out for a brief period of time, so that approximately half of  
25 the amplified DNA remains in the agarose.

40 In a preferred embodiment, the DNA from the colonies may be  
blotted to a CAM membrane, a special membrane that permits reversible  
binding of DNA. CAM is cellulose acetate membrane containing cystamine  
(2,2'-dithio-bis[ethylamine]). The membrane contains primary amino  
45 groups, positively charged below pH 9.5, that can be easily removed under  
mild reductive conditions. CAM has been used to reversibly capture DNA  
fragments separated by electrophoresis. CAM has been successfully used  
with DNA fragments ranging from 0.5 to 320 Kbp. CAMs with different  
50



group densities can be synthesized (up to 1.65  $\mu\text{mole/sq cm}$ ); CAM with 1  $\mu\text{mole amino/sq cm}$  has a binding capacity of at least 10  $\mu\text{g DNA/sq cm}$ . The standard elution conditions for DNA fragments up to 10 Kbp are: 2 hours at room temperature in 25 mM EDTA, 0.2 M NaCl, and 25 mM 2-mercaptoethanol. Larger fragments require higher concentrations of the reducing agent. The chemistry involved in the preparation of CAM is well established (see Sundberg and Porath, *J. Chromatog.* 90:87-98 (1974); Uy and Wolf, (1977)).

CAM is prepared in two steps: (1) Oxirane groups are introduced by reacting cellulose acetate membranes (0.45  $\mu\text{m}$ ) with variable concentrations (0 to 30 % v:v; depending upon the final group density required) of 1,4-butanediol diglycidyl ether in 0.1 M NaOH containing 2 mg/ml sodium borohydride; the reaction is allowed to proceed for 16 hours at RT, with mild agitation. (2) Cystamine is then coupled to the oxirane-containing membrane by reacting with 0.1 M cystamine in 0.1 M sodium tetraborate buffer, pH 9.5, for 16 hours at 37°C. Newly synthesized CAM is fully stable for at least 120 days at 4°C. The content of both oxirane and amino groups can be easily determined by standard reactions.

The thin agarose gel containing amplified DNA molecular colonies may be stained with a sensitive dye such as SIBR-GREEN II (Molecular Probes) in order to localize the position of each colony. The coordinates of the colony position then serves to locate the position of the replicas on the membrane.

In order to recover DNA from a CAM membrane and obtain single-stranded DNA that can be sequenced by standard methods, the procedure is as follows: Molecular colonies are generated as described above to generate single-stranded DNA (embodiment using one specifically structured primer that is inactivated by lowering the temperature), blotted to a CAM membrane, then a small droplet of DNA elution buffer (25 mM EDTA, 0.2 M NaCl, and 25 mM 2-mercaptoethanol) is placed on top of the desired colony, releasing in a few minutes a large proportion of the DNA of that colony replica. The small droplet is then recovered and mixed with four

volumes of a buffer containing a sequencing primer and a suitable sequencing mixture for standard Sanger dideoxy sequencing.

In order to recover DNA from a membrane and regenerate replicatable DNA circles that can be amplified in solution by rolling circle replication, or grown again as molecular colonies, the procedure is as follows: a small droplet of elution buffer (25 mM EDTA, 0.2 M NaCl, and 25 mM 2-mercaptoethanol) is placed on top of the desired colony, releasing in a few minutes a large proportion of the DNA of that colony. The small droplet is then recovered and mixed with four volumes of a buffer containing a restriction enzyme that will cleave the amplified DNA at the rare-cutter site that was designed into the spacer sequence of one of the original PCR primers. After inactivating the restriction enzyme, the DNA is treated very briefly with highly diluted alkaline phosphatase, in order to cause partial dephosphorylation of the termini of the cleaved DNA. After phosphatase inactivation, the DNA is diluted and ligated in the presence of T4 DNA ligase, thus regenerating closed circular molecules. A fraction of the re-circularized molecules will contain a single nick, resulting from dephosphorylated ligation junctions, and these molecules will be capable of initiating rolling circle replication and strand displacement cascade amplification reactions.

#### **Illustration 2: Cloning using a Y-vector**

1. Vector design: This linear vector has a 3' protruding T residue at each end, so as to permit ligation with PCR products that contain a 3'-terminal A (generated during PCR) at each end. The panhandle or tail of the Y is formed by two oligonucleotides that together constitute the second strand of the linear vector. The longer oligonucleotide contains an oligo-dA sequence of 16 bases at the 3' terminus. The oligo-dA sequence serves as an affinity tag (where the affinity target will be oligo-dT). The shorter oligonucleotide contains a 5' phosphate. Sequences of an example of a functional Y-vector are shown below.

K.58 (SEQ ID NO:7)

P-CATGAGGACTAGCAGATGGATGCGGCCGACGCTCG

TGTAATACGACTCACTATAAGGGT-3'

A.60 (SEQ ID NO:8)

P-CCCTATAGTGAGTCGTATTACACGAGCTGCTAGCAT

CATTAGCCAAAAAAAAAAAAAAAAA-3

B.42 (SEQ ID NO:9)

5 P-GGCTAATGATGCTAGGCCGCATCCATCTGCTAGTCCTCATGT-3'

- 10
2. The Y-vector is assembled by incubation of oligonucleotide K.58, A.60 and B.42, for 5 minutes at 40°C, and then ligated with a mixture of PCR-amplicons using T4 DNA ligase at 16°C for 16 hours, to generate
- 15 circular vectors with inserts. Oligonucleotide K.58 is in the first strand (that is, continuous strand) of the circular vector. Oligonucleotides A.60 and B.42 are in the second strand (that is, the discontinuous strand) of the circular vector. Insert sequences are in both strands of the circular vector.
- 20
3. After ligation, the vectors with ligated inserts are incubated at room temperature with oligo-dT-cellulose (Life Sciences, Inc.) in the presence of DNA ligase. The oligo-dT-cellulose is an affinity substrate where the
- 25 cellulose is the solid-state substrate and the oligo-dT is the affinity target. The Y-vector is ligated to the solid matrix via the panhandle sequence (the 5' end of B.42 is covalently bound to the 3' end of the oligo-dT on the oligo-dT-cellulose). The solid matrix is then washed with 20 mM Tris pH 8, 0.1 M NaCl, to remove unligated vectors.
- 30
4. The matrix is washed with 0.5 ml of 50 mM NaOH, releasing single-stranded circular DNA (the first strand of the circular vector) from the cellulose matrix. The now immobilized second strand of the circular vector
- 35 remains attached to the cellulose matrix.
- 25
5. The circular vector is diluted serially to obtain concentrations in the range of several million circular vector molecules per milliliter. Approximately 22 µl of this DNA solution (containing approximately 30,000 to 120,000 DNA molecules) is placed on a cover slip, and covered with a
- 40 polylysine-coated microscope slide. The DNA is allowed to bind to the polylysine-covered surface for 30 minutes at 37°C. The slide then dipped in 0.01% Tween-20, and dried at room temperature.
- 45
- 30

5 6. Using an arraying instrument, an array is constructed consisting of  
6000 individual micro-droplets of a solution containing two suitable primers  
designed for the constant sequence domains of the Y-vector, compatible  
buffer, and polymerase (Large fragment Bst, or exo-Vent DNA polymerase)  
10 5 capable of supporting rolling circle replication.

Primer 1 (23) (SEQ ID NO:10)

GCATCCATCTGCTAGTCCTCATG

Primer 2 (22) (SEQ ID NO:11)

15 CGCAGCTCGTGTAATACGACTC

10 Primer 1 serves as the rolling circle replication primer and a tertiary  
strand displacement primer. Primer 2 serves as a secondary strand  
displacement primer. The use of these primers will result in strand  
20 displacement cascade amplification. The diameter of the droplets should be  
approximately 0.150 to 0.200 millimeters. Droplets are dispensed on the  
15 surface of the slide in a controlled humidity atmosphere, in order to maintain  
a constant droplet volume for a period of 90 minutes. Alternatively, the  
25 diluted circular DNA molecules may be placed on the glass surface using the  
arrayer instrument to dispense small volumes of liquid that on the average  
contain a single ligated DNA molecule.

30 7. The array is incubated for 90 minutes at constant temperature (62°C)  
to amplify any DNA molecules in contact with (or within) the droplets.  
When 33% of the droplets grow DNA colonies, and the rest do not grow  
35 anything, most colonies are likely to be of clonal origin. Adjusting the initial  
inoculum density, it should be possible to obtain up to 1500 clonal colonies  
25 per 6000-droplet array.

40 Optionally, the amplified nucleic acid can be replica plated in order  
to save a copy of the clones or to perform additional operations on the  
clones. In order to facilitate replica plating (via covalent binding to a glass  
surface), each of the two primers used for the strand displacement cascade  
45 30 amplification of the circular vectors may be synthesized with a primary  
amino group at the 5' end. At the end of the SDCA reaction, a glass slide is  
placed over the glass slide with the reaction droplets leaving an air gap of  
less than 1 mm (defined by the thickness of a plastic spacer) in such a  
50

5 manner that the glass on top will contact all of the liquid droplets without  
excessive compression. Prior to use, the lower face of this slide (the upper  
slide) is derivatized using the methods described by Guo *et al.*, *Nucleic Acids*  
10 5 *Research* 22:5456-5465 (1994), and Guo *et al.*, *Nature Biotechnology*  
15:331-335 (1997)), to make the glass surface chemically reactive with  
amino groups. The two-slide sandwich is incubated for 1 to 2 hours at 37°C  
in order to obtain covalent coupling of the amplified DNA contained in each  
droplet to the lower face of the upper slide.

15 8. DNA colonies may be identified by staining with the dye Sybr-  
10 Green-I (Molecular Probes, Inc.). Alternatively, replica slides may be made  
as indicated above, and used for any desired microarray hybridization  
experiment. The DNA in each colony may also be isolated and identified or  
analyzed by DNA sequencing.

## Claims

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I claim:

1. A method of isolating and amplifying a nucleic acid molecule, the method comprising
  - (a) ligating a nucleic acid molecule into a linear vector to form a circular vector comprising the vector and the nucleic acid molecule, wherein the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, wherein the second strand of the circular vector is discontinuous, and wherein the first strand in the circular vector is a closed circular strand,
  - (b) amplifying the first strand by rolling circle replication to form tandem sequence DNA, wherein the amplification results in amplification of the nucleic acid molecule in the first strand.
2. The method of claim 1 wherein the second strand of the linear vector contains at least one nick, wherein the nick cannot be ligated.
3. The method of claim 1 wherein either the 5' or the 3' end of the second strand of the linear vector cannot be ligated.
4. The method of claim 1 wherein the second strand of the linear vector contains at least one gap or overlap.
5. The method of claim 1 wherein the method further comprises, following ligation and prior to amplification, separating the first strand from the second strand.
6. The method of claim 5 wherein the second strand includes an affinity tag.
7. The method of claim 6 wherein the first strand is separated from the second strand by binding the affinity tag to a substrate, denaturing the first and second strands prior to, simultaneous with, or following binding, and separating the first strand from the substrate.
8. The method of claim 5 wherein the second strand of the linear vector contains at least one overlap, part of the overlapping portions of the second strand are complementary, and the 3' end of the overlap extends beyond the part of the overlapping portions that are complementary,

5 wherein the first strand is separated from the second strand by ligating one end of the second strand to a nucleic acid molecule coupled to a substrate, denaturing the first and second strands following ligation of the second strand, and separating the first strand from the substrate.

10 9. The method of claim 1 wherein step (a) comprises ligating a plurality of nucleic acid molecules into a plurality of linear vectors in a single reaction to form a plurality of circular vectors, each circular vector containing at least one nick, gap, or overlap in the second strand.

15 wherein step (b) comprises amplifying the first strand of the plurality of circular vectors, and

20 wherein the method further comprises, prior to amplification, dividing the ligation reaction to produce a plurality of separate amplification reactions.

10. The method of claim 9 further comprising making a replica of the amplification reactions.

25 11. The method of claim 10 wherein the replica of the amplification reactions is made by contacting the amplification reactions with a surface to which nucleic acids can bind.

30 12. The method of claim 10 wherein the replica of the amplification reactions is made by transferring part of each amplification reaction to form a replica amplification reaction.

35 13. The method of claim 9 wherein the ligation reaction is divided by spreading the ligation reaction onto a surface to form a spread, and wherein the separate amplification reactions are the locations of circular vectors on the surface after spreading.

40 14. The method of claim 13 further comprising making a replica of the amplification reactions.

15. The method of claim 14 wherein the replica is made by contacting the spread with a second surface to which nucleic acids can bind.

45 16. The method of claim 9 wherein any number or all of the amplification reactions are ordered as an array of reaction droplets or in an array of reaction vessels.



5 17. The method of claim 16 wherein, following amplification, all or part of the contents of any number or all the individual reaction droplets or reaction vessels are transferred by one to one mapping to a new set of reaction droplets or reaction vessels.

10 18. The method of claim 17 further comprising, following amplification, determining the presence of amplified nucleic acid in the amplification reactions, and

15 transferring all or a part of the contents of the amplification reactions containing amplified nucleic acid reaction to a new set of reaction droplets or reaction vessels.

20 19. The method of claim 16 further comprising making a replica of the amplification reactions.

21. The method of claim 19 wherein the replica of the amplification reactions is made by contacting the amplification reactions with a surface to which nucleic acids can bind.

25 21. The method of claim 19 wherein the replica of the amplification reactions is made by contacting the amplification reactions with a surface treated with an affinity target capable of binding an affinity tag, wherein the amplified nucleic acid comprises affinity tags incorporated during amplification,

30 wherein a portion of each amplification reaction is transferred to the surface.

35 22. The method of claim 21 wherein the affinity tag is biotin and the affinity target is streptavidin.

40 23. The method of claim 21 wherein the affinity tag is a reactive moiety and the affinity target is a corresponding reactive moiety, where a chemical reaction between the affinity tag and the affinity target results in the amplified nucleic acid being covalently coupled to the surface.

45 24. The method of claim 23 wherein the affinity target is phenylene diisothiocyanate, disuccinimidylcarbonate, disuccinimidylsuccinate or dimethylsuberimidate and the affinity tag is a reactive amine.

50 25. The method of claim 19 wherein the replica of the amplification reactions is made by transferring part of each amplification reaction to form a replica amplification reaction.

5           26. The method of claim 16 wherein, following amplification, all or part of the contents of any number or all of the reaction droplets or reaction vessels are transferred and combined to create one or more sets of pooled reactions.

10           27. The method of claim 16 wherein the amplification reactions are arranged on the surface of a substrate.

15           28. The method of claim 27 wherein the substrate comprises acrylamide, cellulose, nitrocellulose, polystyrene, polyethylene vinyl acetate, polypropylene, polymethacrylate, polyethylene, polyethylene oxide, glass, polysilicates, polycarbonates, teflon, fluorocarbons, nylon, silicon rubber, polyanhydrides, polyglycolic acid, polylactic acid, polyorthoesters, polypropylfumerate, collagen, glycosaminoglycans, polyamino acids, chemical resistant metals, or corrosion resistant metals.

20           29. The method of claim 9 wherein the method further comprises, prior to dividing the ligation reaction,

25           diluting the ligation reaction such that, on average, each amplification reaction contains a single circular vector.

30           30. The method of claim 9 wherein the method further comprises, following amplification, collecting a sample of each amplification reaction.

35           31. The method of claim 9 wherein the method further comprises detecting or sequencing the nucleic acid molecules in the amplification reactions or in the collected samples.

40           32. The method of claim 1 wherein rolling circle replication is primed by the second strand.

45           33. The method of claim 1 wherein rolling circle replication is primed by a rolling circle replication primer.

50           34. The method of claim 33 wherein the tandem sequence DNA is amplified by strand displacement replication to form secondary tandem sequence DNA.

55           35. The method of claim 34 wherein the secondary tandem sequence DNA is amplified by strand displacement replication to form tertiary tandem sequence DNA.

          36. The method of claim 34 wherein strand displacement replication of the tandem sequence is primed by a strand displacement primer.

5 37. The method of claim 9 further comprising detecting one or more amplified nucleic acid molecules in one or more of the amplification reactions.

38. The method of claim 37 wherein the nucleic acid molecules are derived from cDNA generated by suppression subtractive hybridization.

10 39. The method of claim 37 wherein the plurality of nucleic acid molecules are all derived from the same source.

40. The method of claim 37 further comprising, following amplification, creating a replica of the amplification reactions,

15 contacting the amplification reactions with a first set of labeled nucleic acid probes and the replica amplification reactions with a second set of labeled nucleic acid probes, and

20 comparing the pattern of hybridization of the first set of probes to the pattern of hybridization of the second set of probes,

wherein differences in the patterns of hybridization indicate differences in the probe sets.

25 41. The method of claim 40 further comprising selecting for isolation or further analysis amplification reactions that

hybridize to the first set of probes but not to the second set of probes, amplification reactions that hybridize to the second set of probes but not to the first set of probes, amplification reactions that hybridize to the both sets of probes, or amplification reactions that do not hybridize to either set of probes.

30 42. An *in vitro* method of cloning nucleic acid molecules, the method comprising

35 (a) dividing a nucleic acid sample to produce a plurality of separate amplification reactions,

(b) amplifying nucleic acid molecules in the amplification reactions,

40 (c) making a replica of the amplification reactions,

(d) testing nucleic acid molecules in either the amplification reactions or the replica amplification reactions to identify nucleic acid molecules of interest,

45 and

(e) retrieving the identified nucleic acid molecules of interest from the corresponding amplification reactions or replica amplification reactions that were not tested.

5 43. The method of claim 42 wherein the nucleic acid sample is divided by spreading the sample onto a surface to form a spread, and wherein the separate amplification reactions are the locations of circular vectors on the surface after spreading.

10 44. The method of claim 43 wherein the replica of the amplification reactions is made by contacting the spread with a second surface to which nucleic acids can bind.

15 45. The method of claim 42 wherein the method further comprises, prior to dividing the nucleic acid sample,

diluting the nucleic acid sample such that, on average, each amplification reaction contains a single nucleic acid molecule.

20 46. A method of isolating and amplifying nucleic acid molecules, the method comprising

(a) ligating a plurality of nucleic acid molecules into a plurality of linear vectors in a single reaction to form a plurality of circular vectors, each circular vector comprising a vector and a nucleic acid molecule,

25 wherein the linear vectors are double-stranded linear nucleic acid comprising two nucleic acid strands, wherein the circular vectors each contain at least one nick, gap, or overlap in the second strand, and wherein the first strand in each circular vector is a closed circular strand,

(b) separating the first strands from the second strands,

35 (c) diluting and dividing the first strands to produce a plurality of separate amplification reactions that, on average, each contain a single circular vector,

(d) amplifying the first strands of the plurality of circular vectors by rolling circle replication to form tandem sequence DNA,

40 wherein the amplification results in amplification of the nucleic acid molecules in the first strands.

45 47. The method of claim 46 wherein the tandem sequence DNA is amplified by strand displacement replication to form secondary tandem sequence DNA.

5           48. The method of claim 47 wherein the secondary tandem sequence DNA is amplified by strand displacement replication to form tertiary tandem sequence DNA.

10           49. A method of isolating and amplifying a nucleic acid molecule, the method comprising

          (a) ligating a nucleic acid molecule into a linear vector to form a circular vector comprising the vector and the nucleic acid molecule,

15           wherein the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, wherein the circular vector contains at least one nick in the second strand and wherein the first strand in the circular vector is a closed circular strand,

20           (b) amplifying the first strand,

          wherein the amplification results in amplification of the nucleic acid molecule in the first strand.

25           50. A kit for isolating and amplifying nucleic acid molecules, the kit comprising

          (a) a linear vector wherein the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, and wherein

30           (1) the linear vector contains at least one nick, wherein the nick cannot be ligated,

          (2) either the 5' or the 3' end of the second strand of the linear vector cannot be ligated,

35           (3) the second strand of the linear vector contains at least one gap,

          (4) the second strand of the linear vector contains at least one overlap, or

40           (5) any combination of (1), (2), (3) or (4);

          (b) a rolling circle replication primer, wherein the rolling circle replication primer is complementary to a portion of the first strand of the linear vector; and

45           (c) a strand displacement primer, wherein the strand displacement primer matches a portion of the first strand of the linear vector.

5 51. A linear vector wherein the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, wherein the second strand of the linear vector contains an affinity tag, and wherein

10 (1) the linear vector contains at least one nick, wherein the nick cannot be ligated,

(2) either the 5' or the 3' end of the second strand of the linear vector cannot be ligated,

15 (3) the second strand of the linear vector contains at least one gap,

(4) the second strand of the linear vector contains at least one overlap, or

(5) any combination of (1), (2), (3) or (4).

20 52. A linear vector wherein the linear vector is a double-stranded linear nucleic acid comprising two nucleic acid strands, and wherein the second strand of the linear vector contains at least one overlap, part of the overlapping portions of the second strand are complementary, and the 3' end of the overlap extends  
25 beyond the part of the overlapping portions that are complementary.

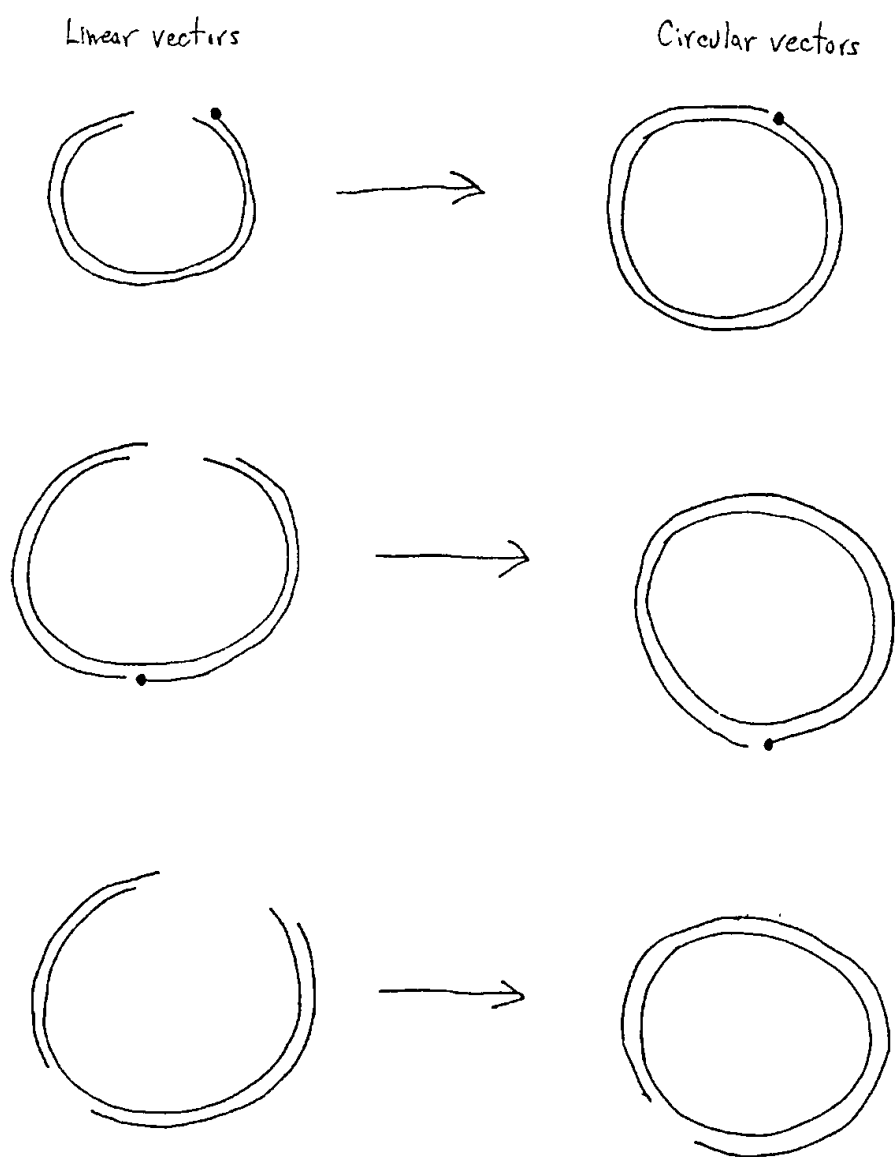


Figure 1A

Figure 1B

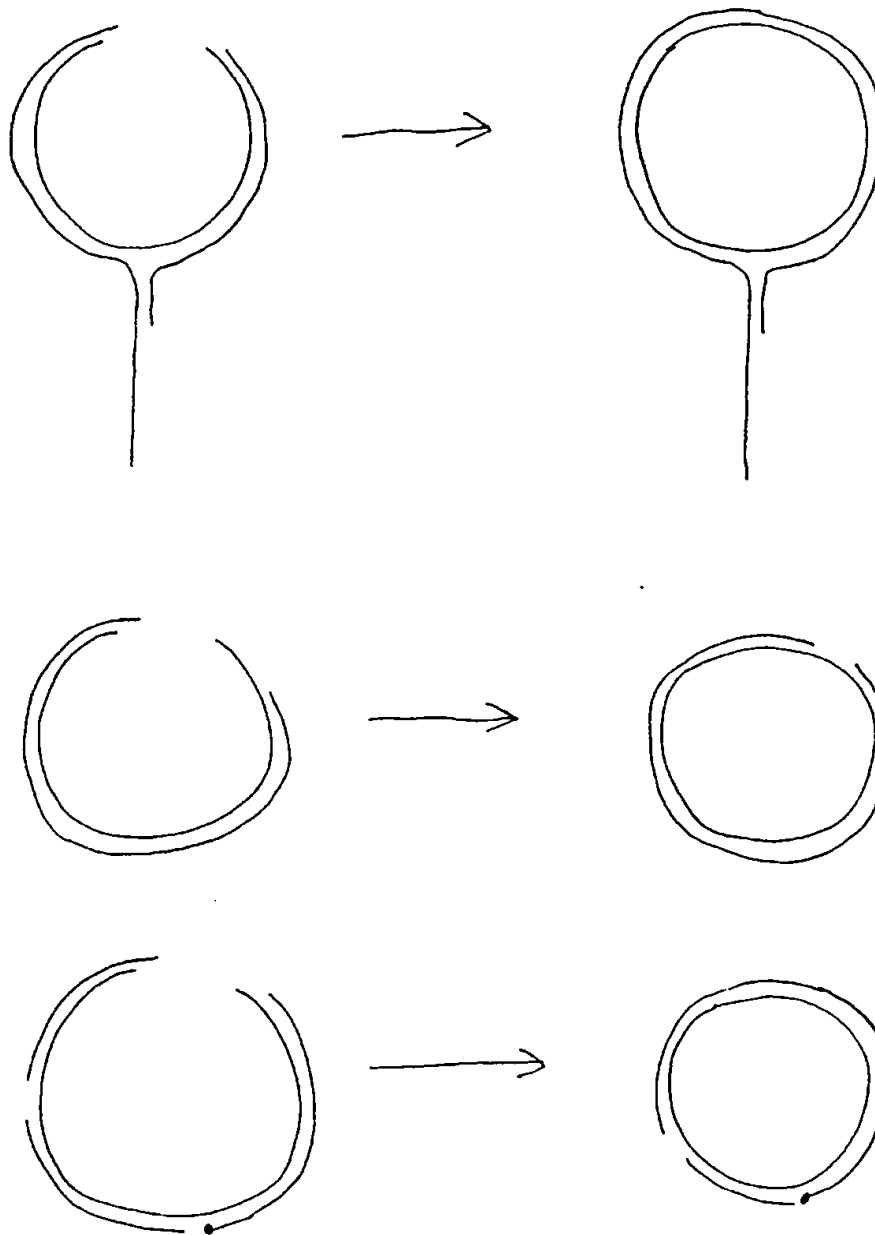




Figure 1C

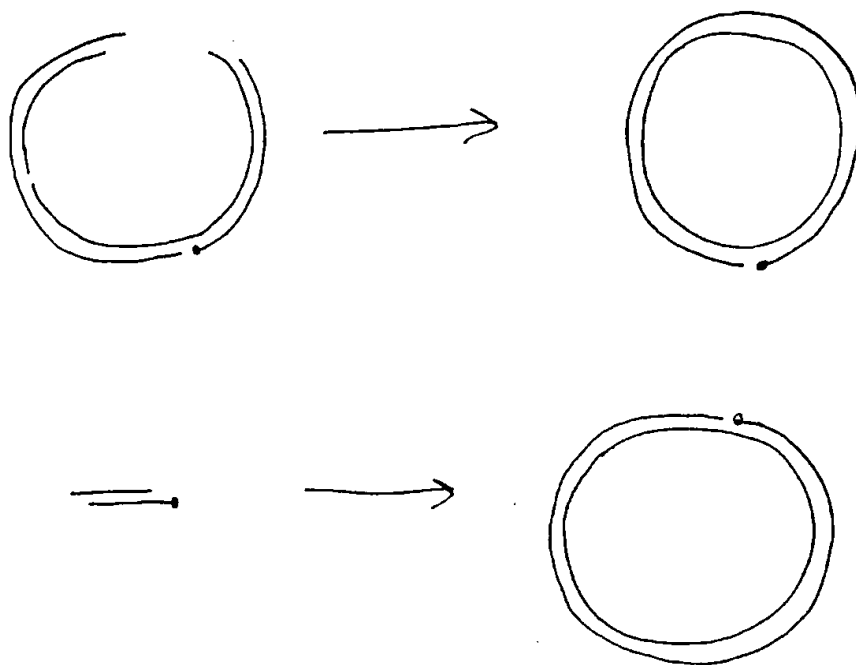


Figure 2A

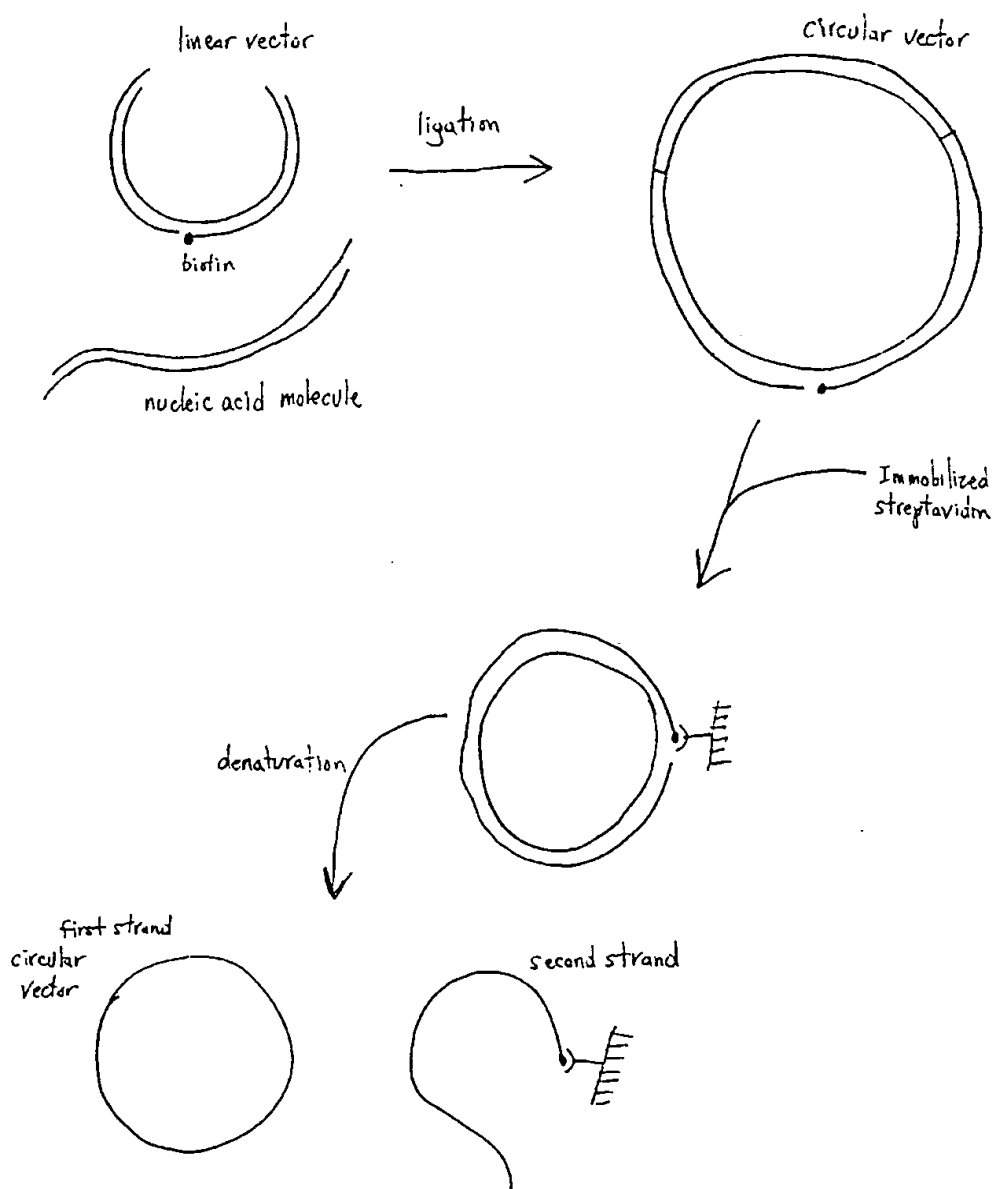
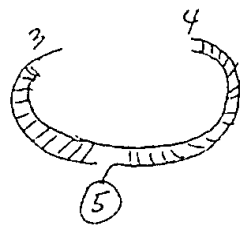
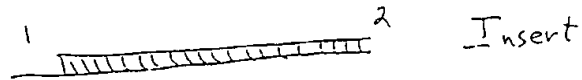
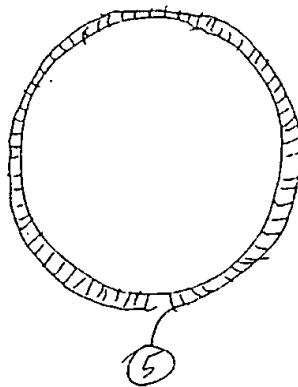


Figure 2B



1, 3 are compatible  
sticky ends  
2, 4 are blunt  
ends



Insert  
has been  
ligated  
into vector

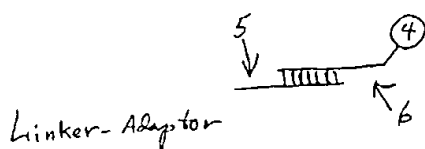
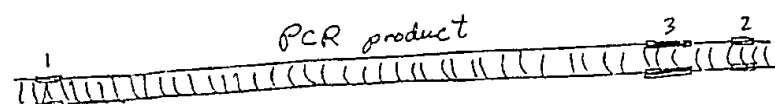
5 is biotin  
or any  
hapten



Figure 4

Primer  
1 →

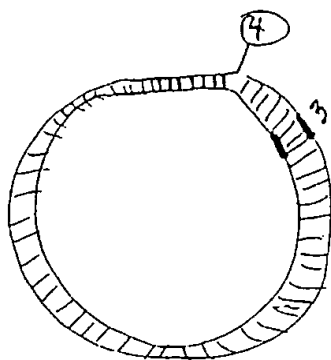
Primer  
← 3 2



1, 2, 3 are restriction sites

5, 6 are sticky ends compatible with 1 and 2

4 is biotin or any hapten



Digested  
PCR  
product  
ligated to  
adaptor

